

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 19, 2003, 16:21:10 ; Search time 82 Seconds

(without alignments)
705.253 Million cell updates/sec

Title: US-09-994-064-11

Perfect score: 2311
Sequence: 1 MRRPHLRKRSRYAKGEVUN.....ACAVLVGLVMSYKCARNS 434

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

1:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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6:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
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9:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
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16:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
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19:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2311	100.0	434	15	AA58856
2	2311	100.0	434	16	AA00638
3	2311	100.0	434	17	AA006790
4	2311	100.0	434	20	AA21984
5	2311	100.0	434	21	AA36040
6	2311	100.0	434	21	AA58184
7	197	8.5	393	10	AA90887
8	190	8.2	369	11	AA06489
9	190	8.2	369	20	AA81601
10	190	8.2	394	5	AA40083

Result No.	Score	Query Match	Length	DB ID	Description
11	189	8.2	394	6	AA50582
12	184.5	8.0	442	13	AA21777
13	179	7.7	388	18	AA11323
14	169	7.7	435	12	AA11273
15	165.5	7.2	308	18	AA11322
16	165.5	7.2	405	12	AA11272
17	165	7.1	402	22	AA878824
18	165	7.1	402	22	AA004969
19	165	7.1	402	22	AA82501
20	165	7.1	973	12	AA14680
21	164	7.1	402	15	AA63142
22	162.5	7.0	373	17	AA96590
23	162.5	7.0	373	21	AA32473
24	162.5	7.0	374	22	AA50118
25	162	7.0	402	8	AA70644
26	161	7.0	402	21	AA07651
27	159	6.9	393	5	AA40084
28	159	6.9	393	18	AA11324
29	158.5	6.9	394	6	AA50581
30	158	6.8	393	19	AA72163
31	158	6.8	400	19	AA72143
32	158	6.8	400	19	AA72013
33	157	6.8	368	16	AA12068
34	156.5	6.8	393	10	AA90748
35	156	6.8	402	22	AA05395
36	151.5	6.6	398	13	AA22322
37	148.5	6.4	417	14	AA37683
38	147.5	6.4	417	14	AA37684
39	144	6.2	417	14	AA37895
40	144	6.2	417	14	AA41345
41	144	6.2	417	16	AA77401
42	144	6.2	417	15	AA75800
43	144	6.2	417	21	AA96087
44	143	6.2	300	22	AA50119
45	142.5	6.2	418	21	AA96086

ALIGNMENTS

RESULT 1
ID AA58856 standard; Protein; 434 AA.

XX	AA58856;
AC	
XX	
DT	13-APR-1995 (first entry)
XX	
DE	Product of gd gene of Infectious laryngotracheitis virus (ILT).
XX	
KW	Homology vector 586-36.6; gd gene; cassette gene.
XX	
OS	Infectious laryngotracheitis virus.
XX	
PN	W09419014-A.
XX	
PD	01-SEP-1994.
XX	
PF	28-FEB-1994; 94MO-US01826.
XX	
PR	26-FEB-1993; 93US-0024156.
XX	
PA	(JAPG) NIPPON ZEON KK.
XX	
PI	(SYTR) SYNTRO CORP.
XX	
XX	Cochran MD;
DR	WPI; 1994-294007/36.
XX	
XX	N-PDB; AA068944.
PT	New recombinant fowl pox virus for use in vaccines - contains
PT	genes expressing antigens of Newcastle disease virus and opt.
PT	Infectious bronchitis virus

Sequence encoded b
EHV-1 envelope gly
HSV glycoprotein D
HSV-1 antigen/heat
HSV glycoprotein D
HSV-1 antigen/heat
Pseudorabies virus
Pseudorabies virus
Pseudorabies virus
HSV surface antige
Glycoprotein 50 (g
Protein decoded fr
DNA encoding fellu
Feline herpesvirus
Pseudorabies virus
Novel recombinant
Sequence of Herpes
HSV glycoprotein D
Sequence encoded b
HSV-2 strain SB5 C
HSV-2 strain SB5 C
HSV-2 strain SB5 C
HSV antigen gD2.
Herpes simplex vir
Pseudorabies virus
Marx Disease Viru
gIV from BHV-1 str
Sequence of a reco
Bovine herpesvirus
BHV1 gIV glycoprot
Bovine herpes viru
Bovine herpesvirus
Feline herpesvirus
Bovine herpesvirus

XX	ILTV; Vaccine; vector; attenuation; poultry;
KW	avian infectious bronchitis virus; Newcastle disease virus;
KW	infectious bursal disease virus of chickens;
KW	Marek's disease virus; herpesvirus; glycoprotein gp.
XX	
OS	Infectious laryngotracheitis virus USDA strain 8302.
XX	
FH	Key
FT	Region
FT	Modified-site
FT	/label= Glycosylation
FT	/note= "potential glycosylation site, but may not
FT	be glycosylated owing to proline residue"
XX	
PN	MO9629396-A1.
PD	26-SEP-1996.
XX	
PF	21-MAR-1996; 96WO-US03916.
XX	
PR	06-JUN-1995; 95US-0468190.
XX	23-MAR-1995; 95US-0410121.
PA	(SYTR) SYNTRO CORP.
XX	
PI	Cochran MD, Wild MA;
XX	
DR	WPI: 1996-443172/44.
DR	N-PSDB; AAT44384;
DR	N-PSDB; AAT44385.
XX	
PT	Recombinant infectious laryngotracheitis virus with deletion in the
PT	glycoprotein G, g1 or US2 gene, etc. - useful for vaccines against
PT	infectious laryngotracheitis in poultry
XX	
PS	Example 11: Page 116-117; 216pp; English.
XX	
CC	Glycoprotein gp (AAM06790) is encoded by ORF7 of the unique short
CC	region (AAT44384) of infectious laryngotracheitis virus (ILTV). It
CC	shows homology to pseudorabies virus 950, and the gp from herpes
CC	simplex virus-1, Marek's disease virus, IPV and bovine herpesvirus
CC	1.1. Expression of gp in vectored fowlpox virus or herpesvirus of
CC	turkeys (HVT) is sufficient to raise a protective immune response
CC	in chickens. ILTV gp expressed in a HVT vector is useful as a
CC	subunit vaccine.
XX	
SSO	Sequence 434 AA;
Query Match	100.0%; Score 2311; DB 17; Length 434;
Best Local Similarity	100.0%; Pred. No. 3,8e-204; Mismatches 0; Gaps 0;
Matches 434;	Conservative 0; Indels 0;
QY	1 MHRPHLRHSRYAAKEVYLNKHMDCGGRKCGAAGVFTLFWTCVIRMRHICFVRNADR 60
DB	1 MHRPHLRHSRYAAKEVYLNKHMDCGGRKCGAAGVFTLFWTCVIRMRHICFVRNADR 60
QY	61 HLFELRNAAWTVTLSSFASSQSTAATVYIIGRRALDALTTPAVGPNYNYLTVRSKGV 120
DB	61 HLFELRNAAWTVTLSSFASSQSTAATVYIIGRRALDALTTPAVGPNYNYLTVRSKGV 120
QY	121 VELNPISNVDDMISAAREKKGPREASVYMEVYVTKGDDGDEKYPPIYKEYREGCDYOL 180
DB	121 VELNPISNVDDMISAAREKKGPREASVYMEVYVTKGDDGDEKYPPIYKEYREGCDYOL 180
QY	181 LSECAVSAQMAVADVSTLVSRRAGALTTFSPALASGYLTLTKIGRFAQTALVTLTE 240
DB	181 LSECAVSAQMAVADVSTLVSRRAGALTTFSPALASGYLTLTKIGRFAQTALVTLTE 240
QY	241 VNRDLKIGSOLNFPSPKSCWTEQVOTGFQGHLPRIADTNRHADDVYRGEDILQRN 300
DB	241 VNRDLKIGSOLNFPSPKSCWTEQVOTGFQGHLPRIADTNRHADDVYRGEDILQRN 300

QY	301	NILRRKNPAPRPDPSPVQOEIPAVTKKKEGRPPDAESSPKKAPPEDEDDMAEASGEN	360
Db	301	NILRRKNPAPRPDPSPVQOEIPAVTKKKEGRIPDAESSKKAPPEDEDDMAEASGEN	360
QY	361	PALPPEDEDEVPEDTEHDDPNSDPDYYNDMPAVIPVEETTKSSNAVSMPIFAFVACAVAL	420
Db	361	PALPPEDEDEVPEDTEHDDPNSDPDYYNDMPAVIPVEETTKSSNAVSMPIFAFVACAVAL	420
QY	421	VGLVWSIVKCAR	434
Db	421	VGLVWSIVKCAR	434
RESULT 4			
ID	AAV21984	standard; Protein; 434 AA.	
AC	AAV21984;		
DT	07-SEP-1999	(first entry)	
DE	Seq ID No: 20 of US5925358.		
KX	Fowlpox virus; FPV; recombinant; vaccine; immunisation; chicken; NDV;		
KW	Newcastle disease virus; NDV; Fowlpox; Infectious Laryngotracheitis.		
OS	Fowlpox virus.		
PN	US5925358-A.		
PD	20-JUL-1999.		
PF	07-JUN-1995;	95US-0484575.	
PR	07-JUN-1995;	95US-0484575.	
PR	26-FEB-1993;	93US-0024156.	
PR	28-FEB-1994;	94MO-US02252.	
PA	(SYTR) SYNTRO CORP.		
PI	Cochran MD, Junker DE;		
DR	WPI: 1999-418249/35.		
DR	N-FSDB; AAX81152.		
XX	Fowlpox viruses, useful as vaccines for immunization of		
XX	chickens/turkeys against Fowlpox and Newcastle disease virus		
XX	Disclosure; column 77-82; 108pp; English.		
XX	The invention relates to a recombinant fowlpox virus (FPV) comprising		
XX	a foreign DNA inserted into a region of the fowlpox virus genome		
XX	corresponding to a 2.8 kb EcoRI fragment, capable of being expressed in a		
XX	host cell. The virus is used as a vaccine for immunising chickens against		
XX	Newcastle disease virus (NDV), Fowlpox, and Infectious Laryngotracheitis.		
XX	Sequence 434 AA.		
XX	SQ		
QY	Query Match	100.0%; Score 2311; DB 20; Length 434;	
Db	Best Local Similarity	100.0%; Pred. No. 3.8e-204;	
XX	Matches 434; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
QY	1	MHRPLRRSRKYAAGEVYLNKMDGCGKRCGGAATFLFWTCVRIMRHICFVRAMDR	60
Db	1	MHRPLRRSRKYAAGEVYLNKMDGCGKRCGGAATFLFWTCVRIMRHICFVRAMDR	60
QY	61	HLFLNNAFWTILYLSFASQSTAAVTYDIILGRALDALITPAVGPNRYLTFVSRGCDV	120
Db	61	HLFLNNAFWTILYLSFASQSTAAVTYDIILGRALDALITPAVGPNRYLTFVSRGCDV	120
QY	121	VELNDISVDDMISAKEKEKGPPEASVYVVIKGDGDEKVCPIYRKEYREGCDV	180
Db	121	VELNDISVDDMISAKEKEKGPPEASVYVVIKGDGDEKVCPIYRKEYREGCDV	180

Db 121 VELNPISNVDDMISAKEKEKGFPEASVYWFYVILKGDGDEDKYCPYRKREYREGCDVQL 180
 QY 181 LSECAVQSAQMAVDPVPTLVSRNGAGLTITSPFAALSGOYLLTLKIGRFAQTALVLE 240
 Db 181 LSECAVQSAQMAVDPVPTLVSRNGAGLTITSPFAALSGOYLLTLKIGRFAQTALVLE 240
 QY 241 VNDRLCKTIGSOLNPLPSKQWTEQYOTGFGHEHLYPIADTNRHADVYRGYEDTLQRMN 300
 Db 241 VNDRLCKTIGSOLNPLPSKQWTEQYOTGFGHEHLYPIADTNRHADVYRGYEDTLQRMN 300
 QY 301 NLIRKKNPSAPDRPDSVPOEIPAVTKKAEGRTPDAESSEKKAPPESEDDMOQAASGEN 360
 Db 301 NLIRKKNPSAPDRPDSVPOEIPAVTKKAEGRTPDAESSEKKAPPESEDDMOQAASGEN 360
 QY 361 PAALPEDEVEPDETHDDPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAAFVACAVAL 420
 Db 361 PAALPEDEVEPDETHDDPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAAFVACAVAL 420
 QY 421 VGLLWMSIVKCAR 434
 Db 421 VGLLWMSIVKCAR 434

RESULT 5
 AAB36040
 ID AAB36040 standard; Protein; 434 AA.

AC AAB36040;
 DT 02-MAR-2001 (first entry)

DE Recombinant fowlpox virus-related polypeptide, SEQ ID NO: 20.

KM Fowlpox virus; FPV; antiviral; antibacterial; vaccine;
 KM Newcastle's disease; Marek's disease; infectious laryngotracheitis.

OS Unidentified.

PN US6136318-A.

PD 24-OCT-2000.

PF 07-JUN-1995; 95US-0486414.

PR 26-FEB-1993; 93US-0024156.

PR 28-FEB-1994; 94MO-US02252.

PA (JUNK/) JUNKER D E.
 PA (COCH/) COCHRAN M D.

XX Cochran MD, Junker DE;

DR WPI; 2000-686071/67.

PT New recombinant fowlpox virus useful as vaccines contains foreign DNA
 PT inserted into specific non-essential region of the genome

PS Disclosure; Column 79-82; 56pp; English.

CC The present sequence is provided in a specification relating to a
 CC recombinant fowlpox virus (FPV) that comprises a foreign DNA inserted
 CC within a 3.5 kb EcoRI fragment of the FPV genomic DNA. The foreign DNA
 CC can be expressed in host cells infected with FPV. The recombinant FPV
 CC may be used in vaccines to protect animals (especially chickens) against
 CC fowlpox and, depending on the source of the foreign DNA, other diseases,
 CC particularly Newcastle's disease, Marek's disease or infectious
 CC laryngotracheitis.

XX Sequence 434 AA;

Query Match 100.0%; Score 2311; DB 21; Length 434;
 Best Local Similarity 100.0%; Pred. No. 3.8e-204;
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRPHLRHRSRYAKGEVNLKHMDCGKRCGAAVFTLMTQVIRIMREHIGFYRAMDR 60
 Db 1 MHRPHLRHRSRYAKGEVNLKHMDCGKRCGAAVFTLMTQVIRIMREHIGFYRAMDR 60
 QY 61 HFLPLRNAFWTIVLLSFAASOSTAAVYDYTLGRRALDALITPAVGPNRYNLTIRVSGCDV 120
 Db 61 HFLPLRNAFWTIVLLSFAASOSTAAVYDYTLGRRALDALITPAVGPNRYNLTIRVSGCDV 120
 QY 121 VELNPISNVDDMISAKEKEKGFPEASVYWFYVILKGDGDEDKYCPYRKREYREGCDVQL 180
 Db 121 VELNPISNVDDMISAKEKEKGFPEASVYWFYVILKGDGDEDKYCPYRKREYREGCDVQL 180
 QY 181 LSECAVQSAQMAVDPVPTLVSRNGAGLTITSPFAALSGOYLLTLKIGRFAQTALVLE 240
 Db 181 LSECAVQSAQMAVDPVPTLVSRNGAGLTITSPFAALSGOYLLTLKIGRFAQTALVLE 240
 QY 241 VNDRLCKTIGSOLNPLPSKQWTEQYOTGFGHEHLYPIADTNRHADVYRGYEDTLQRMN 300
 Db 241 VNDRLCKTIGSOLNPLPSKQWTEQYOTGFGHEHLYPIADTNRHADVYRGYEDTLQRMN 300
 QY 301 NLIRKKNPSAPDRPDSVPOEIPAVTKKAEGRTPDAESSEKKAPPESEDDMOQAASGEN 360
 Db 301 NLIRKKNPSAPDRPDSVPOEIPAVTKKAEGRTPDAESSEKKAPPESEDDMOQAASGEN 360
 QY 361 PAALPEDEVEPDETHDDPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAAFVACAVAL 420
 Db 361 PAALPEDEVEPDETHDDPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAAFVACAVAL 420
 QY 421 VGLLWMSIVKCAR 434
 Db 421 VGLLWMSIVKCAR 434

RESULT 6
 AAV58184

ID AAV58184 standard; Protein; 434 AA.

AC AAV58184;

DT 14-MAR-2000 (first entry)

DE ILTV glycoprotein D (9D).

KM Fowlpox virus; FPV; recombinant; antigenic protein; expression;
 KM infectious laryngotracheitis virus; ILTV; Newcastle disease virus; NDV;
 KM Marek's disease virus; cytokine; promoter; homologous recombination;
 KM homology vector; multivalent; live vaccine; glycoprotein D.

XX Infectious laryngotracheitis virus.

XX US6001369-A.

PN 14-DEC-1999.

PF 07-JUN-1995; 95US-0477459.

PR 26-FEB-1993; 93US-0024156.

PR 28-FEB-1994; 94MO-US02252.

PA (SYTR) SYNTRO CORP.

XX Junker DE, Cochran MD;

DR WPI; 2000-071638/06.

DR N-PSDB; AA49300.

PT Recombinant fowlpox virus useful as a vaccine for immunizing fowl
 PT against Marek's disease, Newcastle disease, infectious
 PT laryngotracheitis virus and/or fowlpox
 PS Claim 5; Columns 79-80; 56pp; English.

XX Herpes Simplex virus-1 gD protein,
DE
XX
XX
vnt Herpes simplex virus-1 gD protein, diagnostic test kit.

XX Polypeptide with activity of surface protein 9D.
DE
XX

[illegible]

```

AC  AAP40083;
XX
XX  12-FEB-1992 (first entry)
XX
DE  Sequence of Herpes simplex virus type 1 gD glycoprotein.
XX
XX  Antigen; vaccine; immunogen.
XX
XX  Herpes simplex virus type 1.
OS
XX
XX  Key Location/Qualifiers
XX  Peptide 1..25
XX  Protein /label= signal
XX  Region 26..394
XX  /label= transmembrane
XX
XX  EPI101655-A.
XX
XX  29-FEB-1984.
XX
XX  19-JUL-1983; 83EP-0401476.
XX
XX  06-JUL-1983; 83US-0510551.
XX  20-JUL-1982; 82US-0400028.
XX  25-OCT-1982; 82US-0436368.
XX  25-JAN-1984; 84US-0573642.
XX
XX  (MOLE-) MOLECULAR GENETICS.
XX  (AMCY) AMERICAN CYANAMID CO.
XX
XX  Watson RJ, Weis JH, Enquist LW;
XX  WPI: 1984-057658/10.
XX  N-PSDB: AAN40070.
XX
XX  Antigenic herpes simplex polypeptide prodn. - by culturing
XX  microorganisms contg. vector including viral DNA fragment
XX
XX  Claim 65; Fig 3; 109pp; English.
XX
XX  The inventors claim: (1) purified DNA sequences coding for the gD
XX  glycoproteins; (2) recombinant DNA vectors contg. these Sqs;
XX  (3) unicellular organisms contg. these DNA Sqs or vectors; and
XX  (4) polypeptides prepd. by these transformed organisms. The pref.
XX  host organism is E.coli ATCC 39139, 39160, B-15451 or B-15471 (see
XX  AAN40070/P40083) or B-15449 or B-15450 (see AAN40071/P40084).
XX
XX  Sequence 394 AA;
XX
Query Match 8.2%; Score 190; DB 5; Length 394;
Best Local Similarity 23.2%; Pred. No. 9.9e-09;
Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

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QY  391 AVIPVEETKSSNAYMPIFAFAVACAVALLVLM 426
DB  342 LI-----AGAVGSLAALVLC-----GIYVM 363

RESULT 11
AAP50582
ID  AAP50582 standard; Protein: 394 AA.
XX
XX  AAP50582;
XX
XX  27-NOV-1991 (first entry)
XX
DE  Sequence encoded by herpes simplex virus -1 (HSV-1) glycoprotein
DE  D (gD) gene.
XX
XX  Glycoprotein; antigen; immunogen; vaccine.
XX
XX  Herpes simplex virus -1.
XX
XX  A08432423-A.
XX
XX  07-MAR-1985.
XX
XX  27-AUG-1984; 84AU-0032423.
XX
XX  09-MAR-1984; 84US-0588170.
XX  30-AUG-1983; 83US-0527917.
XX  31-OCT-1983; 83US-0547551.
XX
XX  (GETH) GENENTECH INC.
XX
XX  Lasky LA, Berman FW;
XX  WPI: 1985-099047/17.
XX  N-PSDB: AAN50489.
XX
XX  Vaccine contg. poly. peptide with exposed antigenic determinants
XX  - useful for giving protection against herpes simplex virus
XX
XX  Example; Fig 1; 93pp; English.
XX
XX  The inventors claim a novel vaccine which contains a membrane-bound
XX  polypeptide having exposed antigenic determinants capable of raising
XX  neutralizing antibodies against a pathogen. Alternatively, the
XX  vaccine contains a truncated membrane-free deriv. The pref.
XX  polypeptide is esp. a glycoprotein of herpes simplex virus types 1
XX  or 2, and the virus is the pathogen. The glycoprotein is a gc and/or
XX  gD. See also A08432424.
XX
XX  Sequence 394 AA;
XX
Query Match 8.2%; Score 189; DB 6; Length 394;
Best Local Similarity 23.5%; Pred. No. 1.2e-08;
Matches 79; Conservative 46; Mismatches 145; Indels 66; Gaps 14;

```

QY 332 RTPEDESSSEKAPDEDESD-MQAEASGENPALPEDEVEDTEHDDPNSDPDYNDMP 390
 DB 284 ETPEMA--TQPELAPDEDESDALLEPVGTVAPQIPPNMHIPEIQDAAPYHPHATPNMG 341
 QY 391 AVIPEETKSSNAVSMPEFAFVACAVALLVW 426
 DB 342 LI-----AGAVGSLALALVTC-----GIYVW 363

RESULT 12
 AAR21777
 ID AAR21777 standard; Protein: 442 AA.
 AC AAR21777;
 XX 10-JUN-1992 (first entry)
 DE EHV-1 envelope glycoprotein D protein.
 KW Equine Herpes Virus-1; g D; vaccination; respiratory;
 XX disease; abortion; neurological disorders.
 OS Equine hepatitis virus.
 FH Key
 FT Cleavage-site 57..58 Location/Qualifiers
 FT Protein /note="cleaves signal peptide" 58..442
 FT Region /label="EHV-1_gd" 80..93
 FT Region /note="peptide 1 - antigenic epitope" 343..361
 FT Modified-site /note="peptide 2 - antigenic epitope" 103..105
 FT Modified-site /note="N-glycosylation site" 111..113
 FT Modified-site /note="N-glycosylation site" 347..349
 FT Modified-site /note="N-glycosylation site" 336..338
 FT Modified-site /note="N-glycosylation site" 405..422
 FT Domain /note="membrane spanning domain"
 PN MQ9202252-A.
 XX 20-FEB-1992.
 PD 25-JUL-1991; 91MO-US05284.
 PF 01-AUG-1990; 90US-0561553.
 PR (RESE) RES CORP TECHN INC.
 PA O'Callaghan DJ;
 PI WPI: 1992-079808/10.
 XX N-PSDB; AAQ21883.
 DR DNA encoding equine herpes virus-1 envelope glyco:protein -
 PT useful in preparation of vaccine composition for immunising
 PT against herpes infection
 XX
 PS Claim 9; Fig 2; 65pp; English.

The equine hepatitis virus-1 envelope glycoprotein D (EHV-1 gd) protein was expressed as a fusion protein with beta-galactosidase using a lambda gt11 expression vector. The resultant recombinant molecules were packaged into lambda phage heads and the phage used to transfect E. coli KM 392 cells in the presence of X-gal. The EHV-1 gd polypeptide was batch purified from the lysate using an anti-beta galactosidase antibody linked to a Sepharose 4-B immuno-affinity column. EHV-1 gd purified in this way was of sufficient

CC purity for production of anti-EHV-1 gd antibodies. The polypeptide
 CC of EHV-1 gd and its fragments are useful in a vaccine compsn. for
 CC passive immunisation of mammals against EHV-1 and hence the associated
 CC respiratory disease, abortions or neurological disorders.
 XX

SQ Sequence 442 AA;
 Query Match 8.0%; Score 184.5; DB 13; Length 442;
 Best Local Similarity 22.1%; Pred. No. 3.8e-08;
 Matches 96; Conservative 59; Mismatches 170; Indels 109; Gaps 20;

QY 18 VLNKMDGCGKRCGSGAAVFTLEWTCVIRMEHCIFRNMMDHLFRNFWITVLLSE 77
 DB 70 ILISVYLSG-----TCKAKRA---VGRQDR----- 93
 QY 78 ASGSTAAVYDY-ILGRALDALITPAVG-----YNRILTVRSRGDVELNPSVDDM 132
 DB 94 -PKVPPRYNYITLITRYNATLVSPINDQVKNVDRLVATRPCEMIALAKTNIDSI 152
 QY 133 ISAKKEKKGPEEASVWVFYIKGDDGEKTC--PIYKREYREGDQVLLSECAVQSAQ 190
 DB 153 LKELAAQKTYR--ARLTWFKIM-----PTCATPIHDVSYMKCKPKLSFAMCDERSDI 203
 QY 191 MNAVDPYSTLVSRNGAGLITFSPALSGOYLTLTKI-GRFAQTALVTLVENDRCITG 249
 DB 204 LMQASLITMAELTDDDELGLVLAAPASAGLYRVRVEIDGRRTYDFSVTIPSEK-PIA 262
 QY 250 SOLNF-LPSKCVTEQYQIG-----FQGEHLPIADITRHAD-----DYRGYEDILQ 297
 DB 263 FELTFGNPCKCTPEQYSKGEVETRRFLGEFNPQGE---HMTWKFEFVYDGGNLPVQ 318
 QY 298 RMNMLRKKMPSAPDPRP--DSVPEIIPAVTKAEERTDASSSEKAPPEDESDMAE 355
 DB 319 FYEGQAFAR-PVPPDHPHGFDSVESL-----TQNKTDPKGQADPKRN 361
 QY 356 ASGENPA---ALPEDEVEDTEHDDPNSDPDYNDMPAVIPEETKSSNAVSMPIFAA 412
 DB 362 QPFKMPISIKHLVRLDEVEYTE-----PTKPKP--TKSNSNTEFGISVG 405
 QY 413 FVACAVALLVGLVW 426
 DB 406 LGIAGLVGLVILY 419

RESULT 13
 AAM11323
 ID AAM11323 standard; Protein: 388 AA.
 AC AAM11323;
 XX 29-APR-1997 (first entry)
 DE HSV glycoprotein D variant gd-1(delta290-299).
 DE HSV glycoprotein D variant; gd-1(delta290-200); antiviral;
 KW virucide.
 OS Herpes simplex virus type 1 strain Patton.
 FH Key
 FT Peptide 1..25 Location/Qualifiers
 FT Protein /label="sig_peptide" 26..388
 FT /note="Mat. protein of the wild-type gd-1 replaced by Arg-Lys-Ile-Phe"
 PN W09703199-A1.
 XX 30-JAN-1997.
 PD 03-JUL-1996; 96MO-US11344.

XX HSV; glycoprotein D variant; gd-1(del290-200t); antiviral;
KW virucide.
XX
OS Chimeric herpes simplex virus type 1 strain Patton;
OS Chimeric Apis sp.;
OS Chimeric synthetic.
XX
FH Key
FT 1..2
FT Peptide
FT /label= Sig-peptide
FT /note= "fragment of honeybee mellitin signal
FT peptide, left following expression of
FT the variant gd-1 in Sf9 cells"
FT
FT Protein
FT 3..308
FT /label= "Mat protein
FT /note= "the mature protein has amino acids 290-299
FT of the wild-type gd-1 replaced by
FT Arg-Lys-Ile-Phe, and amino acids 308-399
FT replaced by 5 His residues"
XX
XX WO9703199-A1.
XX
XX 30-JAN-1997.
XX
XX 03-JUL-1996; 96WO-US11344.
XX
XX 07-JUL-1995; 95US-0499568.
XX
XX (COMP-) COMPETITIVE TECHNOLOGIES INC.
XX
XX Cohen GH, Eisenberg RJ, Nicola A;
XX
XX WPI; 1997-119054/11.
XX N-PDB; AAT51317.
XX
XX Variant Herpes Simplex virus glycoprotein D molecule - contains
XX mutation in region IV of the glycoprotein, used for inhibiting
XX infection of susceptible cells by HSV
XX
XX Claim 1; Page 23-24; 57pp; English.
XX
XX A variant herpes simplex virus (HSV) glycoprotein D (AAM11322),
XX designated gd-1(del290-299t), is the product of recombinant
XX expression in Sf9 cells of a fusion protein including the honeybee
XX mellitin signal peptide and Patton strain HSV-1 gd in which Patton
XX strain mature gd-1 amino acid residues 290-299 (in region IV) are
XX replaced by Arg-Lys-Ile-Phe and residues 308-369 (transmembrane
XX region) by 5 His residues. A DNA sequence encoding the variant gd
XX is given in AAT51317. Region IV of gd-1 is required for entry of HSV
XX into susceptible cells. The gd-1 variant has potent antiviral
XX activity and can be used to prevent or ameliorate HSV infection.
XX
XX Sequence 308 AA;
SQ

Query Match 7.2%; Score 165.5; DB 18; Length 308;
Best Local Similarity 23.4%; Pred. No. 1.2e-06;
Matches 66; Conservative 33; Mismatches 122; Indels 61; Gaps 10;

OY 106 PYNRLTRVSRGCDVVELNPNVDMISAAKEKEGPFEEASVYFYIKGDDGDDKXC 165
DB 56 PITYVYAVLERACRSYLVNAPSEAPQIVGASEDVAKOPYNLTIAFRM-----GNCAT 110
OY 166 PIYKREYRCGIVQLISECAVOSAOMWAVDYPS-TLVSRNGAGLTTFSPTAALSGOYLL 224
DB 111 PITYVMEYECSSYNKSLGACPIRTOPRM--NYDSFSAVSEDMIGFLMHAPAFETAGTYLR 168
OY 225 TLKIGFAOTALVLTLE--VNDRCCLKIGSOLNPLPSKCWTTEBOYOTGFOGEHLIPIADINT 282
DB 169 LVKINDMTETITQFIIFHRAKSGC-KYALPLRIPSPACUSPOAYQGQVTVDSIGML----- 222
OY 283 RHADDVRYGEDIILRWNNLLRKNKNSAPDPRDSVPOEIPAVT-----KKAGRTPPDAES 338

DB 223 -----PRFIPENQRYAVVSLKTAGMHGPKAPY 250
OY 339 SEKKAPPEDEDDMQAEASGENPALPDEDEVPEDTE-HDDP 379
DB 251 TSTLLPELSE-----TPNATQPELAPED--PEDSALLDDP 284

Search completed: February 19, 2003, 16:23:31
Job time : 84 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 19, 2003, 16:21:10 ; Search time 21 Seconds

(without alignments)
1986.778 Million cell updates/sec

Title: US-09-994-064-11

Perfect score: 2311
Sequence: 1 MRPHLRHSRYAKGEVLN.....ACAVLVGLWISYKACARS 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.73:*

1: pirl:1:1
2: pirl:2:1
3: pirl:3:1
4: pirl:4:1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	190.5	8.2	393	1	VGEBDZ
2	190	8.2	394	1	glycoprotein D - h
3	190	8.2	394	1	glycoprotein D - h
4	187	8.1	394	1	glycoprotein D pre
5	181	7.8	442	1	glycoprotein D pre
6	175	7.6	452	1	glycoprotein D pre
7	165	7.1	402	1	glycoprotein D pre
8	158	6.8	393	1	glycoprotein D pre
9	158	6.8	393	2	glycoprotein D pre
10	156.5	6.8	393	1	glycoprotein D - h
11	148.5	6.4	380	2	glycoprotein D - h
12	146	6.3	402	2	glycoprotein D - h
13	146	6.3	402	2	glycoprotein D - h
14	144	6.2	417	1	glycoprotein D pre
15	139.5	5.7	384	2	glycoprotein D pre
16	131.5	5.6	498	1	glycoprotein D pre
17	129	5.6	498	1	glycoprotein D pre
18	116	5.0	976	2	glycoprotein D pre
19	113.5	4.9	307	2	glycoprotein D pre
20	108.5	4.7	395	1	glycoprotein D pre
21	106.5	4.6	509	2	glycoprotein D pre
22	106.5	4.6	501	2	glycoprotein D pre
23	106	4.6	727	2	glycoprotein D pre
24	106	4.6	764	2	glycoprotein D pre
25	105.5	4.6	2499	1	glycoprotein D pre
26	105	4.5	574	2	glycoprotein D pre
27	104.5	4.5	1643	2	glycoprotein D pre
28	104.5	4.5	2911	2	glycoprotein D pre
29	104.5	4.5	3381	2	glycoprotein D pre

30	104	4.5	539	2	T15871	hypothetical prote
31	103	4.5	300	2	T02220	hydroxypoline-ric
32	103	4.5	708	2	D96711	hypothetical prote
33	103	4.5	727	2	S18193	autoantigen NOR-90
34	103	4.5	764	2	S09318	transcription fact
35	103	4.5	1881	2	H95076	zinc metalloprote
36	103	4.5	7962	2	T38346	elastic titin - hu
37	103	4.5	26926	1	T38344	titin, cardiac mus
38	102.5	4.4	416	1	SKXLAG	dermal gland prote
39	102.5	4.4	856	2	T16543	hypothetical prote
40	101	4.4	651	2	S18874	nucleolin - Africa
41	101	4.4	727	2	JC5113	ribosomal transcr
42	101	4.4	764	2	JC5112	ribosomal transcr
43	101	4.4	855	2	D98004	histidine Motif-Co
44	101	4.4	1211	2	T42230	Af4 protein - mous
45	101	4.4	1277	2	T14152	synaptic scaffold

ALIGNMENTS

RESULT 1

glycoprotein D precursor - human herpesvirus 1 (strain Hst)

C:Species: human herpesvirus 1

C>Date: 31-Dec-1993 #sequence: revision 31-Dec-1993 #text-change 09-Sep-1994

C:Accession: A90945; A03729

R:Jasky, L.A.; Dowbenko, D.J.

DNA 3, 23-29, 1984

A:Title: DNA sequence analysis of the type-common glycoprotein-D genes of herpes s1m1

A:Reference number: A90945; MUID:84131549; PMID:6321120

A:Accession: A90945

A:Molecule type: DNA

A:Residues: 1-393 <LAS>

A:Cross-references: GB:K02372

C:Superfamily: herpesvirus glycoprotein D

C:Keywords: glycoprotein; transmembrane protein

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-393/Product: glycoprotein D #status predicted <TM>

F:341-360/Domain: transmembrane #status predicted <TM>

F:118,145,286/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.2%; Score 190.5; DB 1; Length 393;

Best Local Similarity 23.3%; Pred. No. 4.1e-07;

Matches 80; Conservative 49; Mismatches 139; Indels 75; Gaps 15;

QY	99	LTTPAVGPNRYLTVRSRGCDVVELNPISNVDMISAKEKEGPEASVYVTKGD	158
DB	80	ITVYAV-----LEKACRSVLLNAPSEAPQIVRGASEDVRRKQVNLITAFRM----	126
QY	159	DGEDKYPPIYRKREYREGCDVQLSECAVQSAQMAVDVYPS-ILVSRNGAGLTIESPTAA	217
DB	127	-GGCAAPITVMEYTECSYNSKSLGACPIRQPRW--NYYSFSAVSVDNIGFLHMAFAFE	183
QY	218	LSGGVLLTKIGRPAQALVTL--VNDRCIKISOLNPLPSKQMTQOTG-----	268
DB	184	TAGTYLLVKNINDTETTGTFLEHRAKGC-KYALPIRPSACLSQAQOQGVTVDSIG	242
QY	269	----FOGHHLPYIADTTRHADVDYRGYEDILQWNNLTKRKNSAPDPSPDQPIPA	324
DB	243	MLPFRITENQRTVAVYSLKTIAG-----WH-----GPRAP-YSTLLPPLP-	282
QY	325	VTKAAGRTPDAAESSEKAPPEDESD-MQAEASGEPALPPEDEVDPEDEHDPSP	383
DB	283	-----ETPNA--TQELAPBEDPESALLEDVGTVAPOIPRMWILPSIDQATPYHP	333
QY	384	DYVNDMPAVTVPEETTKSSNVAWPIFAFVACAVLVGLVW	426
DB	334	ATPNNMGLT-----ACAVGSLALALVTC-----GIYIW	362

Query Match

Best Local Similarity 23.28; Score 190; DB 1; Length 394;
Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

Query 106 PYNRYLTVRSRCDDVYELNPISNVDMISAKKEKGPFPAASVYVFIKGDGEDKXC 165
Db 79 PITYVYAVLERACRSVYLLNAPSEAPQIVRGASEDRKOPYMLTIAMFRM-----GNCAL 133
QY 166 PIYKREYRECGDQVLLSECAVQSAQMAVADYVS-TIVSRNAGLITFSPTAALSGOYL 224
Db 134 PITVAEYTEGCSYKSLGACPIRTQPRM--NYDSFSAVSEDNLFGLHMAPEFAGTYLR 191
QY 225 TLKIGRFQOTALVYLE--VNDRCILKIGSQLNLPDSKWTTEYOYQTG-----FOG 271
Db 192 LKTIKDWTEIQFIIEHRAKGC-KYALPLRIPSCACISPAQYQGVTVDSIGMLPFPIR 250
QY 272 EHLPIADTNRHADVDYRGYEDILQRRNNLLRKNNSAPDRPDSVPOELPAVTKAEG 331
Db 251 ENQRTVAAYSLKING-----WH-----GKAP-YISTLLRPEL-----S 283
QY 332 RTPPAESEKKAPPEDESD-MQAEASGENPAPLPEDDEVPEDETHDDPSPDYYNDMP 390
Db 284 ETPNA--TQPLAEDPEDSALIEDPVGVAQLPQRMHILPSIQDATPPIHPRATPTNNMG 341
QY 391 AVIPEETTKSSNMPIFAAFACAVCALVGLIYW 426
Db 342 LI-----AGAVGSGSLAALVYC-----GLIYW 363

RESULT 4

A4/627
glycoprotein D precursor - human herpesvirus 1 (strain ANG)
C/Species: human herpesvirus 1
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C/Accession: A4/627
R/izumi, K.M.; Stevens, J.G.
J. Exp. Med. 172, 487-496, 1990
A/Title: Molecular and biological characterization of a herpes simplex virus type 1 (C)
A/Reference number: A4/627; MUID:90324869; PMID:2165127
A/Accession: A4/627
A/Molecule type: DNA
A/Residues: 1-394 <I20>
C/Cross-references: GB:X54361; NID:960414; PIDN:CA38245.1; PID:960415
C/Superfamily: herpesvirus glycoprotein D
C/Keywords: glycoprotein; transmembrane protein
F.11-20/Domain: signal sequence #status predicted <SIG>
F.21-394/Product: glycoprotein D #status predicted <GPD>
F.342-360/Domain: transmembrane #status predicted <TMN>
F.119,146,287/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 8.18; Score 187; DB 1; Length 394;
Matches 77; Conservative 46; Mismatches 155; Indels 50; Gaps 14;

QY 106 PYNRYLTVRSRCDDVYELNPISNVDMISAKKEKGPFPAASVYVFIKGDGEDKXC 165
Db 79 PITYVYAVLERACRSVYLLNAPSEAPQIVRGASEDRKOPYMLTIAMFRM-----GNCAL 133
QY 166 PIYKREYRECGDQVLLSECAVQSAQMAVADYVS-TIVSRNAGLITFSPTAALSGOYL 224
Db 134 PITVAEYTEGCSYKSLGACPIRTQPRM--NYDSFSAVSEDNLFGLHMAPEFAGTYLR 191
QY 225 TLKIGRFQOTALVYLE--VNDRCILKIGSQLNLPDSKWTTEYOYQTG-----FOG 271
Db 192 LKTIKDWTEIQFIIEHRAKGC-KYALPLRIPSCACISPAQYQGVTVDSIGMLPFPIR 250
QY 272 EHLPIADTNRHADVDYRGYEDILQRRNNLLRKNNSAPDRPDSVPOELPAVTKAEG 331
Db 251 ENQRTVAAYSLKING-----WH-----GKAP-YISTLLRPEL-----S 283
QY 332 RTPPAESEKKAPPEDESD-MQAEASGENPAPLPEDDEVPEDETHDDPSPDYYNDMP 390
Db 284 ETPNA--TQPLAEDPEDSALIEDPVGVAQLPQRMHILPSIQDATPPIHPRATPTNNMG 341
QY 391 AVIPEETTKSSNMPIFAAFACAVCALVGLIYW 426
Db 342 LI-----AGAVGSGSLAALVYC-----GLIYW 363

Qy 340 EKKAPDESEDD-MQAEASGENPALPEDDEVEDTEHDDPNSDPDYNDMPAVIPVET 398
 Db 290 QPELAPDEPEDSALLEDDVGVYAPQIPPMWHIPSTODATPAPHPATPNNGLI----- 343
 Qy 399 TKSSNAVSMPIFAFVACAVALLV 426
 Db 344 ---AGAVGSLALALVIC-----GLVW 363

RESULT 5

VGBEBA

glycoprotein D precursor - equine herpesvirus 1 (strain Kentucky A)

C:Species: equine herpesvirus 1
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
 C:Accession: A38518
 R:Flowers, C.C.; Eastman, E.M.; O'Callaghan, D.J.
 Virology 180, 175-184, 1991
 A:Title: Sequence analysis of a glycoprotein D gene homolog within the unique short segment
 A:Reference number: A38518; MUID:91082407; PMID:1845821
 A:Accession: A38518
 A:Molecule type: DNA
 A:Residues: 1-442 <FLO>
 A:Cross-references: EMBL:M62923; NID:G330892; PIDN:AAA46081.1; PID:G330893
 C:Superfamily: herpesvirus glycoprotein D
 C:Keywords: glycoprotein; transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-442/Product: glycoprotein D #status predicted <MAT>
 F:404-422/Domain: transmembrane #status predicted <TM2>
 F:103,111,347,396/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.8%; Score 181; DB 1; Length 442;
 Best Local Similarity 23.0%; Pred. No. 2,66-06;
 Matches 84; Conservative 56; Mismatches 153; Indels 72; Gaps 17;

Qy 87 YDY-ILGRALDALITPAVG---YNYLTRVSRGCDVVELNPISNVDMISAKEK 141
 Db 102 YNYTLITRYNATLALSPINDQVKNVDLRIVATPRCEMIALIAKTINDISILKELAOK 161
 Qy 142 GGPFAASVWVFYVTKGDDGEKTC--PIYKREYRCGVQLSCEAVASQAQMAVDYPS 199
 Db 162 --TYSARLTWFKIM-----PTCATPIHDVSYMKCNPKLSFAMCDESDILMOASLT 212
 Qy 200 TLVSRNGALITFPTALSGQYLTLTKI-GRFAQTALVTLEVNDRCIKISQINF-LPS 257
 Db 213 AAEFDDELGLVLAAPAHASGLYRIVTIDGRRIYDPSVTIPSRG-PIAFELNFGMPD 271
 Qy 258 KCMTEGYOTG-----FOGELHYPIADTNTRHAD---DVRGVEDILQRMNMLRK 306
 Db 272 RCKTPEQYSGREVFTRRLGFEFNGPGE---HMTWKFVYVDS-GMLPVQFYEAQFA 326
 Qy 307 NPSAPDPRP--DSVPQELPAVTKAEGTTPAESSEKKAPDESEDDMQAEASGENPA-- 362
 Db 327 RVPVDPNHPGDVSESEI-----TQNTDKPKGQADPKPQOPKMPK 370
 Qy 363 -ALPEDDEVPEDTEHDDPNSDPDYNDMPAVIPVEETTKSSNAVSMPIFAFVACAVALL 421
 Db 371 HLVPRLEDDVEVIE-----PVTKPKP--TSKSNSTFVIGISVGLGIALVLV 414
 Qy 422 GLVW 426
 Db 415 GVILY 419

RESULT 6

VGBE3

glycoprotein D precursor - equine herpesvirus 1

C:Species: equine herpesvirus 1
 A:Note: host Equus caballus (domestic horse)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Jul-1999
 C:Accession: I36802; B36646; PQ0146
 R:Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
 submitted to Genbank, March 1992

A:Description: The DNA sequence of equine herpesvirus-1.
 A:Reference number: A36805
 A:Accession: I36802
 A:Molecule type: DNA
 A:Residues: 1-452 <TEL>
 A:Cross-references: G8:M6664; NID:G330791; PIDN:AA802507.1; PID:G330863
 R:Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
 Virology 189, 304-316, 1992
 A:Title: The DNA sequence of equine herpesvirus-1.
 A:Reference number: A41831; MUID:92295566; PMID:1318606
 A:Contents: annotation; possible protein-coding frames
 A:Note: neither amino acid nor nucleotide sequence is given
 R:Adonnet, J.C.; Winslow, J.; Allen, G.; Proletti, E.
 J. Gen. Virol. 71, 2969-2978, 1990
 A:Title: Equine herpesvirus type 1 unique short fragment encodes glycoproteins with
 A:Reference number: A36646; MUID:91108393; PMID:2177089
 A:Accession: B36646
 A:Molecule type: DNA
 A:Residues: 1-452 <AUD>
 A:Cross-references: G8:M6664; NID:G330791; PIDN:AA802507.1; PID:G330863
 A:Experimental source: strain Kentucky D
 R:Elton, D.M.; Halliburton, I.W.; Killington, R.A.; Meredith, D.M.; Bonass, W.A.
 Gene 101, 203-208, 1991
 A:Title: Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine herpesv
 A:Reference number: JQ0998; MUID:91276272; PMID:1647359
 A:Accession: PQ0146
 A:Molecule type: DNA
 A:Residues: 292-452 <ELT>
 A:Cross-references: G8:M6299; NID:G330787; PIDN:AAA66546.1; PID:G808672
 C:Genetics:
 A:Gene: 72
 C:Superfamily: herpesvirus glycoprotein D
 C:Keywords: glycoprotein; transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-452/Product: glycoprotein D #status predicted <MAT>
 F:399-419/Domain: hydrophobic <HYD>
 F:404-422/Domain: transmembrane #status predicted <TM2>
 F:103,111,347,396/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:347,396/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.6%; Score 175; DB 1; Length 452;
 Best Local Similarity 22.6%; Pred. No. 7,96-06;
 Matches 84; Conservative 53; Mismatches 149; Indels 86; Gaps 17;

Qy 87 YDY-ILGRALDALITPAVG---YNYLTRVSRGCDVVELNPISNVDMISAKEK 141
 Db 102 YNYTLITRYNATLALSPINDQVKNVDLRIVATPRCEMIALIAKTINDISILKELAOK 161
 Qy 142 GGPFAASVWVFYVTKGDDGEKTC--PIYKREYRCGVQLSCEAVASQAQMAVDYPS 199
 Db 162 --TYSARLTWFKIM-----PTCATPIHDVSYMKCNPKLSFAMCDESDILMOASLT 212
 Qy 200 TLVSRNGALITFPTALSGQYLTLTKI-GRFAQTALVTLEVNDRCIKISQINF-LPS 257
 Db 213 AAEFDDELGLVLAAPAHASGLYRIVTIDGRRIYDPSVTIPSRG-PIAFELNFGMPD 271
 Qy 258 KCMTEGYOTG-----FOGELHYPIADTNTRHADVYRGYEDILQRMNMLRK 305
 Db 272 RCKTPEQYSGREVFTRRLGFEFNGPGEHMT-----MLKFWFYVYDGLVLPVQF 319
 Qy 306 -----KNPSAPDPRP--DSVPQELPAVTKAEGTTPAESSEKKAPDESEDDMQAEAS 357
 Db 320 YEAQAFARVPPDNHPCGVSESEI-----TQNTDKPKGQADPKPQOPKMP 363
 Qy 358 GENPA--ALPEDDEVPEDTEHDDPNSDPDYNDMPAVIPVEETTKSSNAVSMPIFAFV 414
 Db 364 FKWPSIKHLAPRLDEVEVIE-----PVTKPKP--TSKSNSTFVIGISVGLG 407
 Qy 415 ACAVALVGLVW 426
 Db 408 IAGLVAVGVILY 419

```

RESULT 7
VGBE50
glycoprotein D precursor - suid herpesvirus 1 (strain R1ce)
C:Species: suid herpesvirus 1
A:Note: host Sus scrofa domestica (domestic pig)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jul-1999
C:Accession: A27788
J:Petkovsis, E.A.; Timmins, J.G.; Armentrout, M.A.; Marcholt, C.C.; Yancey Jr., R.J.;
J. Virol. 59, 216-223, 1986
A:Title: DNA sequence of the gene for pseudorabies virus gp50, a glycoprotein without N-
A:Reference number: A27788; MUID:86281819; PMID:3016293
A:Molecule type: DNA
A:Residues: 1-402 <PEP>
A:Cross-References: GB:M4001; NID:9334051; PIDN:AAG3203.1; PID:9334052
C:Superfamily: herpesvirus glycoprotein D
C:Keywords: glycoprotein; transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-402/Product: glycoprotein D #status predicted <GPD>
F:362-376/Domain: transmembrane #status predicted <TM>

Query Match 7.1%; Score 165; DB 1; Length 402;
Best Local Similarity 21.0%; Pred. No. 4e-05;
Matches 88; Conservative 55; Mismatches 139; Indels 118; Gaps 19;

OY 73 ILSSASOSTAATVTDYILG-----RRALDALTPAVGPNRYLNR-VSRG 117
DB 6 LLAALVARTTGADVDAVAPPTPPPAYPTESMQLTLTVPSFPGADVHTRPLEDP 65
OY 118 CDVVELNPISNVDDMISAKEREKGGPEASVWVYVYKGGDEKCP--TYREKREC 175
DB 66 CGVVALISDPQVDRLNAAVAHRR-PTIRAHVAMTRIADG-----CAHLTYFIEYADC 117
OY 176 GDVQLISCAVQSAQW---ADVVPSTLVSRNGAGLTIFSPALSGQY--LLETKIGR 230
DB 118 DPROVFGRCRRRTTPMWTSPADYMFPT---EDELGLIMVAPGFNGQRLRLVSDGVN 174
OY 231 FAQALVLELVNDRCLTKISQNLPLPSKWTQEQYOTGFQGHLYPIADYTRADYV 288
DB 175 ILTFMVALLPREGQCPARVQHTYKFGACWSDSTFRGV-----PSAPPRPSVP 319
OY 289 YR-----GYEDILQRMNNLLRKNN-----PSAPPRPSVP 319
DB 218 MRFLPTPYQOPPHREYVNYW---YRKNGRTLPRHAHAATPYAIDPARPSAGSPRRPRR 273
OY 320 QETPAVTKKAGRTPPDAESSEKAPRED--SEDMQAASENPAALPEDEVEDTEHDD 378
DB 274 RPRPRKPEPAPATP-----APPRLPEPATROHAGGRTPPRPRPEPH-----R 320
OY 379 PNSDPDYNDMPAVT-----PVEETKSSNAVS---MPFAAFVACAVLVGLLVW 426
DB 321 PFAP-----PAVPSGMPQPAEPQPTPPAPGVSRHSRYIVGTGMAGALLVGVCV 373

RESULT 8
VGBE33
glycoprotein D precursor - human herpesvirus 2 (strain 333)
C:Species: human herpesvirus 2
A:Note: host Homo sapiens (man)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C:Accession: A03732
R:Watson, R.J.
Gene 26, 307-312, 1983
A:Title: DNA sequence of the herpes simplex virus type 2 glycoprotein D gene.
A:Reference number: A03732; MUID:84159516; PMID:6323270
A:Molecule type: DNA
A:Residues: 1-393 <MAT>
A:Cross-References: GB:K01408; NID:9330268; PIDN:AAA5841.1; PID:9330269
C:Superfamily: herpesvirus glycoprotein D
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>

```

```

F:25-393/Product: glycoprotein D #status predicted <GPD>
F:340-356/Domain: transmembrane #status predicted <TM>
F:119,146,287/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 6.8%; Score 158; DB 1; Length 393;
Best Local Similarity 19.9%; Pred. No. 0.00014;
Matches 69; Conservative 55; Mismatches 152; Indels 70; Gaps 12;

OY 97 DALTPAVGPNRYLTVRSRCGVDELNPISNVDDMISAKEREKGGPEASVWVYVYK 156
DB 71 DPQPPST-PTTYVAVLERACRSVLLHAPSEAPQIVRGASDARHNTYLLTAWYRM-- 127
OY 157 GDGDEKPCPLTYREYRECGDVQLISCAVQSAQWAVDVVPSTLVSRNGAGLTIFSPA 216
DB 128 ---GDNCALPTTWETPEYCKNSLGVCPTRTOPRMSY--YDSFSAVSEDLGFLMAHAPAF 183
OY 217 ALSGQVLLTKIGFAQTALVTVLEVNDRCLTKISQNLPLPSKWTQEQYOTGFQGHLY 275
DB 184 ETAGTYRLVKINDWPEITQFLEHRAHRSCKALPLRLPPACLTLSKAYQOGVTVDSIG 243
OY 276 PIADYTRHADYVYRGEDILQRMNNLLRKKNPSADPPRDSVPOEIPAVT-----KKAEG 331
DB 244 ML-----PRIPENQRTVALYSKIAGW 266
OY 332 RTPDAESSEKAPPESEDDMQAASENPAALPEDEVEDTE-HDDP-----NSDPD 384
DB 267 HGKRPPTSTLLPELSD---TTNATQPELVPEP---PESALLEDPEAGTVSSQIIPN 318
OY 385 YVNDMPAVIPV---EETKSSNAVSMPJFAAFVACAVLVGLLVW 426
DB 319 WH--IPSIDVAPHHNAPARNPNSGLITGALASTIALAVTIGIAVW 362

RESULT 9
E43674
US6 protein - human herpesvirus 2 (strain H652)
C:Species: human herpesvirus 2
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: E43674
R:McGeoch, D.J.; Moss, H.W.M.; McNab, D.; Frame, M.C.
J. Gen. Virol. 68, 19-38, 1987
A:Title: DNA sequence and genetic content of the HindIII 1 region in the short unique
A:Reference number: E43674; MUID:87111457; PMID:3027242
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-393 <MG>
A:Cross-References: EMBL:X04798
C:Superfamily: herpesvirus glycoprotein D

Query Match 6.8%; Score 158; DB 2; Length 393;
Best Local Similarity 20.3%; Pred. No. 0.00014;
Matches 71; Conservative 53; Mismatches 148; Indels 78; Gaps 13;

OY 97 DALTPAVGPNRYLTVRSRCGVDELNPISNVDDMISAKEREKGGPEASVWVYVYK 156
DB 71 DPQPPST-PTTYVAVLERACRSVLLHAPSEAPQIVRGASDARHNTYLLTAWYRM-- 127
OY 157 GDGDEKPCPLTYREYRECGDVQLISCAVQSAQWAVDVVPSTLVSRNGAGLTIFSPA 216
DB 128 ---GDNCALPTTWETPEYCKNSLGVCPTRTOPRMSY--YDSFSAVSEDLGFLMAHAPAF 183
OY 217 ALSGQVLLTKIGFAQTALVTVLEVNDRCLTKISQNLPLPSKWTQEQYOTGFQGHLY 275
DB 184 ETAGTYRLVKINDWPEITQFLEHRAHRSCKALPLRLPPACLTLSKAYQOGVTVDSIG 243
OY 276 PIADYTRHADYVYRGEDILQRMNNLLRKKNPSADPPRDSVPOEIPAVT-----KKAEG 331
DB 244 ML-----PRIPENQRTVALYSKIAGW 266
OY 332 RTPDAESSEKAPPESEDDMQAASENPAALPEDEVEDTE-HDDP-----NSDPD 384

```

QY 71 IVLLSSFASQSTAAVTYDYILGRALDAL TIPAVGPYNRYLTR--VSRGCDVEELNPIS 127

```
Db 291 ESEITONKTN--PKOEASPKPNPFKWPSSIKOLAPRIDEVDNAK---EITTKKPPASN 34
```

Db 291 ESEITQNKTN--PKQEQASPKPNPFKWPISIKQLAPRIDEVDNAK---EITTKKPPASN 34

OY 348 S 348
Db 345 S 345

RESULT 13

Probable glycoprotein D - equine herpesvirus 4 (strain NS80567)

C:Species: equine herpesvirus 4

A:Virus: strain NS80567

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000

C:Accession: T42615

R:Telord, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.

J. Gen. Virol. 79, 1197-1203, 1998

A:Title: The DNA sequence of equine herpesvirus-4.

A:Reference number: 222173; PMID:98264497; PMID:9603335

A:Accession: T42615

A>Status: preliminary; translated from GB/EMBL/DDJ

A:Molecule type: DNA

A:Residues: 1-402 <TEL>

A:Cross-references: EMBL:AF030027; NID:g2605950; PIDN:AAC59592.1; PID:g2606020

A:Experimental source: strain NS80567

C:Genetics:

A:Note: 72

C:Superfamily: herpesvirus glycoprotein D

Query Match

Best Local Similarity 22.3%; Score 146; DB 2; Length 402;

Matches 67; Conservative 38; Mismatches 120; Indels 76; Gaps 13;

OY 94 RALALTPAVGPNRYLRSRCGVNELNPISNDMTSAKEKEGPEASVMEY 153

Db 75 KIVYKTVAAIRP-----CEMALIALAKTNVDSIIKELDAHK--TYSARLTWFK 121

OY 154 VIKGDDEDKYC--PIYKEYREGCDVQLSECAVQSAQMAVADVSTLVSRGAGLTI 211

Db 122 I-----PTCATPIHIDVYMKNPRLFGMCDERENITLITTAETDDELGLVL 174

OY 212 FSPALASGOYLTLTKL-GPFAQTALVLEVNDRCIKIGSQLNF-LPSKQWTEOYQYG- 268

Db 175 ASPAHSTYSGLYRRVLIQIDGRRYITDFSVTLPSHC-PLSFQNGFNPDRCRTEOYSRGE 233

OY 269 -----FOGELH-----YPLADTYTRADYVYRG 291

Db 234 VYTSRFLSEFNYRGVILAVKMFVQDGNLVQYFEAQAFAFPVPPDHHGEFDSV--- 290

OY 292 YEDILQRMNNLLRKKNSAPDRP---DSVPOEIPAVTKKAGRTPDASSEKKAAPED 347

Db 291 ESEITONKTN--PKQEQASPKPMPFPKWPISIKQLAPRIDEVDMAK-----EITTKKPPASV 344

OY 348 S 348

Db 345 S 345

RESULT 14

glycoprotein D precursor - bovine herpesvirus 1 (strain P8-2)

C:Species: bovine herpesvirus 1

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999

C:Accession: A36548

R:TIKOO, S.K.; Fitzpatrick, D.R.; Babluk, L.A.; Zamb, T.J.

J. Virol. 64, 5132-5142, 1990

A:Title: Molecular cloning, sequencing, and expression of functional bovine herpesvirus

A:Reference number: A36548; MUID:90376470; PMID:2168991

A:Accession: A36548

A:Molecule type: DNA

A:Residues: 1-417 <TIK>

A:Cross-references: GB:M59846; NID:g330745; PIDN:AAA6050.1; PID:g330746

C:Superfamily: herpesvirus glycoprotein D

C:Keywords: glycoprotein; transmembrane protein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-417/Product: glycoprotein D #status predicted <MAN>
F:361-369/Domain: transmembrane #status predicted <TMN>
F:41,102/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 23.1%; Score 144; DB 1; Length 417;

Matches 79; Conservative 47; Mismatches 156; Indels 60; Gaps 17;

OY 109 RYLTVRSRCGVNELNPISNDMTSAKEKEGPEASVMEYIKGDGDKYC--P 166

Db 67 RYATSA--ACDMLLALIDPQVGRITLWEAVRRH--ARAVNAIVYWKIESG-----CARP 117

OY 167 IYRKEYREGCDVQLSECAVQSAQMAVADVSTLVSRGAGLTIPTALSGOYLTL 226

Db 118 LYMEIYECPEKPKHFGICRTITPFWDSFLAGRAVPTDDELGLIMAPARLVGQYRRAL 177

OY 227 KI-GPFAQT-ALVYLEVNDRC-LKIGSQLNLFPSKQWTEOYQ-----TGF--Q 270

Db 178 YIDGTVAYTDFMVSFLPAGD-CWFSKLGAGRYTFGACFPARQYEQKVLRLTYLTQYRQ 236

OY 271 GEHLIPLADTYTRADY-----YKGYEDILQRMNNLLRKKNSAPDRPDSVPOEIPA 324

Db 237 EAHKAIIVDYWMKRGVVPYFEESSKGYE-----PPAADGSPAPPDDBA 283

OY 325 VTKKAEGRTPD-AESSEKKAAPEDSEDDMQAASGENPALPEDEVPDTEHDNDSP- 382

Db 284 --KDEGETEDGAGREGNGGPPGPDGSESTPEANGGAGEPKRGP-----SPDAOR 335

OY 383 PDYINDMPAVI---PVEETTKSSNAYSMPLEAFVACAAVALY- 421

Db 336 PEGWPSLEAITHPAPATPAADAVPAGVIGIIMAAALACV 377

RESULT 15

glycoprotein gd - bovine herpesvirus 1

C:Species: bovine herpesvirus 1

C:Date: 09-Jun-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999

C:Accession: S35784

R:Audonnet, J.

submitted to the EMBL Data Library, June 1993

A:Reference number: S35782

A:Accession: S35784

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-417 <AUD>

A:Cross-references: EMBL:Z23068; NID:g312185; PIDN:CAAB0604.1; PID:g312188

C:Superfamily: herpesvirus glycoprotein D

C:Keywords: glycoprotein

Query Match

Best Local Similarity 22.2%; Score 139.5; DB 2; Length 417;

Matches 88; Conservative 41; Mismatches 179; Indels 89; Gaps 16;

OY 58 MDRHLFLRNAEWTIVLSSFSQSTAAVYDYLGRALDLALTPAVGPNRYLTVSRG 117

Db 37 MPRVNYTERMHTTGPISPFADGRQPEVRYAASAAACDMLALIDPQVGRITLWEAVR- 95

OY 118 CDVVELNPISNDMTSAKEKEGPEASVMEYIKGDGDKYC--PIYKEYREC 175

Db 96 -----RHARAANAIVYWKIESG-----CARPLYMEYEYEC 126

OY 176 GDVQLSECAVQSAQMAVADVSTLVSRGAGLTIPTALSGOYLTLTKL-GPFAQT 234

Db 127 EPRKHFQGRKRTITPFWDSFLAGRAVPTDDELGLIMAPARLVGQYRRALYIDGVAYT 186

OY 235 -ALVYLEVNDRC-LKIGSQLNLFPSKQWTEOYQYGFGGELH-----YF-----I 277

Db 187 DFMWLPAGD-CWFSKLGAGRYTFGACFPARQYEQKVLRLTYLTQYRQ 242

OY 278 AD-INTRADY-----YKGYEDILQRMNNLLRKKNSAPDRPDSVPOEIPA 330

Db 243 VDIWMRHRGAVVPYFEESSKGYE-----PPAADG-----GSPAPPDDE 282

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 19, 2003, 16:21:10 : Search time 13 seconds

(Without alignments)
1384.671 Million cell updates/sec

Title: US-09-994-064-11

Perfect score: 2311

Sequence: 1 MRRPHLRHRRHYAKGEVLN.....ACAAVLGLWWSIVKCAR 434

Scoring table:

BLOSUM62

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	196	8.5	393	1	VGLD_HSV1H
2	190	8.2	393	1	VGLD_HSV1H
3	190	8.2	394	1	VGLD_HSV1P
4	187	8.1	394	1	VGLD_HSV1A
5	181	7.8	442	1	VGLD_HSVEX
6	175	7.6	402	1	VGLD_HSVEX
7	175	7.6	452	1	VGLD_HSVEX
8	165	7.1	402	1	VGLD_HSV2
9	156.5	6.8	393	1	VGLD_HSV2
10	144	6.2	417	1	VGLD_HSVBP
11	139.5	6.0	380	1	U114_HSVNG
12	139.5	6.0	417	1	VGLD_HSVBS
13	129	5.6	498	1	VGKX_PVRRI
14	118.5	5.1	1311	1	GAK_HUMAN
15	116	5.0	976	1	XPR6_YARLI
16	108.5	4.7	395	1	VGLD_HSVSB
17	105	4.6	764	1	UBF1_HUMAN
18	105.5	4.6	2499	1	UBF1_RAT
19	104.5	4.5	3381	1	PGCV_BOVIN
20	104	4.5	539	1	YOK2_CAEEL
21	103	4.5	426	1	ASD4_NEUCR
22	103	4.5	764	1	UBF1_HUMAN
23	102.5	4.4	278	1	OSTP_SHEEP
24	102.5	4.4	439	1	XP2_XENLA
25	101	4.4	650	1	NUCL_XENLA
26	100.5	4.3	1121	1	MYT1_HUMAN
27	100	4.3	969	1	SACB_STRSL
28	99.5	4.3	765	1	UBF1_MOUSE
29	98.5	4.3	1131	1	YAB9_YEAST
30	97.5	4.2	393	1	CALX_CANFA
31	97.5	4.2	651	1	MEU6_SCHPO
32	97	4.2	359	1	A2HS_BOVIN
33	97	4.2	499	1	RRG_BRAE

34	97	4.2	533	1	G19P_BOVIN
35	97	4.2	793	1	NETB_DROME
36	97	4.2	859	1	DD24_HUMAN
37	96.5	4.2	503	1	STZ_BPSP
38	96	4.2	489	1	DMP1_RAT
39	96	4.2	2175	1	HMCU_DROME
40	95.5	4.1	174	1	EGD2_YEAST
41	95.5	4.1	1782	1	Y044_UREPA
42	95.5	4.1	1953	1	BIGA_SALT
43	95.5	4.1	2472	1	NCR2_MOUSE
44	95	4.1	591	1	CALX_RAT
45	94.5	4.1	311	1	OSTP_RABIT

ALIGNMENTS

RESULT 1

VGLD_HSV1H STANDARD: PRT: 393 AA.

AC P06476; 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Glycoprotein D precursor.

GN CD OR US6.

OS Herpes simplex virus (type 1 / strain HZT).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Simplexvirus.

OX NCBI_TaxID=10305;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=84131549; PubMed=6321120;

RA Lasky L.A., Dowlenko D.J.;

RT "DNA sequence analysis of the type-common glycoprotein-D genes of

herpes simplex virus types 1 and 2."

RL DNA 3:23-29(1984).

CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,

CC GB, GC, GD, GI, GT AND GE.

CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to license@isb-sib.ch).

CC EMBL: K02372; AAA45786.1; -.

DR PIR: A90945; VGBED2.

DR InterPro: IPR002896; Herpes_glycop.D.

DR Pfam: PF01537; Herpes_glycop.D.1.

KW Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 25

FT CHAIN 26 393

FT DOMAIN 26 338

FT TRANSMEM 339 363

FT DOMAIN 364 393

FT DOMAIN 364 380

FT SIGNAL 1 25

FT CHAIN 26 393

FT DOMAIN 26 338

FT TRANSMEM 339 363

FT DOMAIN 364 393

FT DOMAIN 364 380

FT SIGNAL 1 25

FT CHAIN 26 393

FT DOMAIN 26 338

FT TRANSMEM 339 363

FT DOMAIN 364 393

FT DOMAIN 364 380

FT SIGNAL 1 25

FT CHAIN 26 393

FT DOMAIN 26 338

FT TRANSMEM 339 363

FT DOMAIN 364 393

FT DOMAIN 364 380

Query Match 8.54; Score 196; DB 1; Length 393;
Best Local Similarity 24.08; Pred. No. 1.6e-07;
Matches 79; Conservative 46; Mismatches 138; Indels 66; Gaps 14;

113 RVSGCDVLENPISNVDMISAKEKGGPFASVWVFVIGDDGDEKCYPTIRKEY 172

```

Db      85 RVERACRSVLLNAPSEAPQIVRGASEDYRKQPYNLTIAMFRM-----GCNCALPITVMEY 139
QY      173 RRCGVOLLSECAVOSAGMMAVDYPS--TLVSRNGAGLTIFSPALSGOYLTKIGRF 231
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      140 TCCSNKSLGACPIRTQPRM--NYDSFSAVSEDNIGFLMHAPAPETAGTYLRKINDW 197
QY      232 AOTALVTLF--VNDRLKIGSQLNPLPSKCWTTEQYGTG-----FQGHLYPIA 278
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      198 TEITOFILFHRAGKSC-KYTLPLRIPPSACLSPOAYQGVYVDSIGMLPRFIPEKQRTVA 256
QY      279 DNTNHHADVYRGYEDIIQRMNNLLRKNPSAPDRPDSVQOEIPAVTKKAGRTPDAS 338
      257 VYSLTIAG-----WH-----GPRAP-VTSTLLPPELP-----ETPNA-- 287
QY      339 SEKKAPPEDESD--MOEASGENPALPEDEVPEDTEHDDPNSDPDYNDMPAVIPEE 397
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      288 TOPELAPPEDESDALDEPVGTVAPQIIPNMHIPSIDAPAPYHHPATPNMGLI----- 342
QY      398 TTKSSNAVSMPIFAAFVACAVALVGLVW 426
      343 ---AGAVGSLAALVLC-----GIYVW 362

```

RESULT 2

VGLD_HSV11

AC Q69091; P03171; 012833; 012544; PRT; 394 AA.

DT 21-JUL-1986 (Rel. 01, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Glycoprotein D precursor.

GD OR US6.

OS Herpes simplex virus (type 1 / strain 17).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Simplexvirus.

NCBI_TaxID=10299;

[1]

SEQUENCE FROM N.A.

RX MEDLINE=85160822; PubMed=2964429;

RA McGeoch D.J., Dolan A., Donald S., Rixon F.J.;

RT "Sequence determination and genetic content of the short unique region

J. Mol. Biol. 181:1-13(1985).

[2]

REVIEWS.

RA McGeoch D.J.;

RL Submitted (JAN-1989) to the EMBL/Genbank/DBJ databases.

CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,

GB, GC, GD, GI, AND GE.

CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.

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CC EMBL: L00036; AAA96682.1; -

DR EMBL: X14112; CAA32283.1; -

DR PIR: A03730; VGBEL7.

DR InterPro: IPR002896; Herpes_glycop_D.

DR Pfam: PF01537; Herpes_glycop_D.1.

KW Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 25 POTENTIAL.

FT CHAIN 1 25 GLYCOPROTEIN D.

FT DOMAIN 26 394 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 340 364 POTENTIAL.

FT DOMAIN 365 394 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 365 381 ARG/LYS-RICH (HIGHLY BASIC, PROBABLY

SERVES TO ANCHOR THE GLYCOPROTEIN IN

THE MEMBRANE).

FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 394 AA; 43346 MW; 94852171F355F6FC CRC64;

Query Match 8.28; Score 190; DB 1; Length 394;

Best Local Similarity 23.28; Pred. No. 4.5e-07;

Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

```

QY      106 PYNRYLFRVRCGVNVLNPLNSVNDWIMISAKEKEGCEPEASVWVYVYKGDGDEKTC 165
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      79 PITYYAVLBERACRSVLLNAPSEAPQIVRGASEDYRKQPYNLTIAMFRM-----GCNCAL 133
QY      166 PIYREYRECGVOLLSECAVOSAGMMAVDYPS--TLVSRNGAGLTIFSPALSGOYL 224
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      134 PITYMEYTECSYNKSLGACPIRTQPRM--NYDSFSAVSEDNIGFLMHAPAPETAGTYLR 191
QY      225 TLKIGRAQALVTLF--VNDRLKIGSQLNPLPSKCWTTEQYGTG-----FQGH 271
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      192 LVKINDTEITQFILERAGKSC-KYALPLRIPPSACLSPOAYQGVYVDSIGMLPRFI 250
QY      272 EHLYPADVTNTRHADVYRGYEDIIQRMNNLLRKNPSAPDRPDSVQOEIPAVTKKAG 331
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      251 ENQRTVAVYSLKTAG-----WH-----GPRAP-VTSTLLPPELP-----ETPNA-- 283
QY      332 RTPDASSSEKKAPPEDESD--MOEASGENPALPEDEVPEDTEHDDPNSDPDYNDMP 390
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      284 ETPNA--TOPELAPPEDESDALDEPVGTVAPQIIPNMHIPSIDAPAPYHHPATPNMNG 341
QY      391 AVIPVEETKSSNAVSMPIFAAFVACAVALVGLVW 426
      342 LI-----AGAVGSLAALVLC-----GIYVW 363

```

RESULT 3

VGLD_HSV1P

AC P57083; P03171; STANDARD; PRT; 394 AA.

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Glycoprotein D precursor.

GD OR US6.

OS Herpes simplex virus (type 1 / strain Patton).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Simplexvirus.

NCBI_TaxID=10308;

[1]

SEQUENCE FROM N.A.

RX MEDLINE=83016630; PubMed=6289440;

RA Watson R.J., Weiss J.H., Salstrom J.S., Englund L.W.;

RT "Herpes simplex virus type-1 glycoprotein D gene: nucleotide sequence

Science 218:381-384(1982).

CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,

GB, GC, GG, GD, GI, AND GE.

CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.

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CC EMBL: X02138; CAA26060.1; -

DR EMBL: J02217; AAA45785.1; -

DR PIR: A03729; VGBEL7.

DR InterPro: IPR002896; Herpes_glycop_D.

DR Pfam: PF01537; Herpes_glycop_D.1.

KW Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 25 POTENTIAL.

FT CHAIN 26 394 GLYCOPROTEIN D.
 FT DOMAIN 26 339 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 340 364 POTENTIAL.
 FT DOMAIN 365 394 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 365 381 ARG/LYS-RICH (HIGHLY BASIC; PROBABLY
 SERVES TO ANCHOR THE GLYCOPROTEIN IN
 THE MEMBRANE).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 394 AA; 43346 MW; 052ABB5F303D5E CRC64;

Query Match 8.2%; Score 190; DB 1; Length 394;
 Best Local Similarity 23.2%; Pred. No. 4.5e-07;
 Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

QY 106 PYNRYLTVRSRGCDVVELNPISNVDMISAKEKEKGFPEASVYWFYIKGDGEDKYYC 165
 DB 79 PITVYVAVLERACRSVLLNAPSEAPQIVRGSEDEVKQPYMLTAMFRM-----GNCAL 133
 QY 166 PIYKREYREGCDVOLLSCAVQSQMMAVDYVPS-TLYSRNAGAGLTITSPALSGOYLL 224
 DB 134 PITVMEYTESYKNSLGCAPRTQPRW--NYDSFSAVSEDLGFLMAPEFETAGTYLR 191
 QY 225 TLKIGRFAOTLVTLE--VNDRCIKIGSQLNPLPSKWTBOYGTGFGH---LYPIAD 279
 DB 192 LKINDWEITQFLEHRAKSC-KYALPLRIPSAISPAYQGVYVDSIGMLPRIP 250
 QY 272 EHLPIADTNRHADVDYRGYEDILQRMNNLRKKNPSAPRDPSPQELPAVTKAEG 331
 DB 251 ENQRTAVVSLKING-----WH-----GPKAP-YTSTLLPEL-----S 283
 QY 332 RTPAESSEKAPRDESD-MQAEASGENPALPEDEVEDTEHDDNSPDYNDMP 390
 DB 284 ETPNA--TQPELAPEDPSALLEDVGTVAQIIPNMHPISTQDAATPYHPATPNNGLI----- 343
 QY 391 AVIPEETTKSSNAVSMPIFAAFVACAVALLVLMW 426
 DB 342 LI-----AGAVGSLALALVYC-----GIYWM 363

RESULT 4

VGDL_HSV1A STANDARD; PRT; 394 AA.

AC P36318; 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glycoprotein D precursor.
 GN GP OR US6.

OS Herpes simplex virus (type 1 / strain Angelotti).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OX NCBI_TaxID=10301;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-90324869; PubMed-2165127;
 RA Izumi K.M., Stevens J.G.;
 RT "Molecular and biological characterization of a herpes simplex virus
 type 1 (HSV-1) neuroinvasive gene.";
 RL J. Exp. Med. 172:487-496(1990).

CC -I- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,
 CC GB, GC, GG, GD, GI, AND GE.
 CC -I- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.

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DR EMBL; X54361; CAA38245.1; .
 DR PIR; A47627; A47627; Herpes-glycop-D.
 DR InterPro; IPR002896; Herpes-glycop-D; 1.
 DR Pfam; PF01537; Herpes-glycop-D; 1.
 KW Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 25
 FT CHAIN 26 394 GLYCOPROTEIN D.
 FT DOMAIN 26 339 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 340 364 POTENTIAL.
 FT TRANSMEM 365 394 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 365 381 ARG/LYS-RICH (HIGHLY BASIC; PROBABLY
 SERVES TO ANCHOR THE GLYCOPROTEIN IN
 THE MEMBRANE).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 394 AA; 43303 MW; 47DE3BC79B828950 CRC64;

Query Match 8.1%; Score 187; DB 1; Length 394;
 Best Local Similarity 23.5%; Pred. No. 7.6e-07;
 Matches 77; Conservative 46; Mismatches 155; Indels 50; Gaps 14;

QY 106 PYNRYLTVRSRGCDVVELNPISNVDMISAKEKEKGFPEASVYWFYIKGDGEDKYYC 165
 DB 79 PITVYVAVLERACRSVLLNAPSEAPQIVRGSEDEVKQPYMLTAMFRM-----GNCAL 133
 QY 166 PIYKREYREGCDVOLLSCAVQSQMMAVDYVPS-TLYSRNAGAGLTITSPALSGOYLL 224
 DB 134 PITVMEYTESYKNSLGCAPRTQPRW--NYDSFSAVSEDLGFLMAPEFETAGTYLR 191
 QY 225 TLKIGRFAOTLVTLE--VNDRCIKIGSQLNPLPSKWTBOYGTGFGH---LYPIAD 279
 DB 192 LKINDWEITQFLEHRAKSC-KYALPLRIPSAISPAYQGVYVDSIGMLPRIP 250
 QY 280 TNRHADVDYRGYEDILQRMNNLRKKNPSAPRDPSPQELPAVTKAEGRTPDAES 339
 DB 251 ENQ-----IVAVVSLKINGW-----GPKAP-YTSTLLPEL-----SETPNA--T 289
 QY 340 EKKAPRDESD-MQAEASGENPALPEDEVEDTEHDDNSPDYNDMPAIVPDET 398
 DB 290 QPELAPEDPSALLEDVGTVAQIIPNMHPISTQDAATPYHPATPNNGLI----- 343
 QY 399 TKSSNAVSMPIFAAFVACAVALLVLMW 426
 DB 344 ---AGAVGSLALALVYC-----GIYWM 363

RESULT 5

VGDL_HSVK STANDARD; PRT; 442 AA.

AC P22484; 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glycoprotein D precursor (Glycoprotein 17/18).
 GN GP OR GP17/18 OR 72.

OS Equine herpesvirus type 1 (strain Kentucky A) (EHV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 OX NCBI_TaxID=10329;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-91082407; PubMed-1845821.
 RA Flowers C.C., Eastman E.M., O'Callaghan D.J.;
 RT "Sequence analysis of a glycoprotein D gene homolog within the unique
 RT short segment of the EHV-1 genome.";
 RL Virology 180:175-184(1991).
 RN [2]

CC SEQUENCE FROM N.A.
 RX MEDLINE-92263758; PubMed-1316673;
 RA Colie C.F., Iii, Flowers C.C., O'Callaghan D.J.;
 RT "Open reading frames encoding a protein kinase, homolog of
 RT glycoprotein gx of pseudorabies virus, and a novel glycoprotein map

RT Within the unique short segment of equine herpesvirus type 1.;

RL Virology 188:545-557(1992).

CC -I- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.

CC -----

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CC -----

DR EMBL: M62923; AAA46081.1; -

DR EMBL: M87931; -; NOT_ANNOTATED_CDS.

DR EMBL: M87937; AAA46073.1; ALT_INIT.

DR PIR: A38518; VGBEEA.

DR InterPro: IPR002896; Herpes_glycop_D.

DR Pfam: PF01537; Herpes_glycop_D; 1.

DR Glycoprotein; signal: Transmembrane.

FT SIGNAL 1 19 POTENTIAL.

FT CHAIN 1 19 POTENTIAL.

FT DOMAIN 20 442 GLYCOPROTEIN D.

FT TRANSMEM 406 422 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 423 442 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 442 AA; 49908 MW; 323CDA9C96762F05 CRC64;

Query Match 7.8%; Score 181; DB 1; Length 442;

Best Local Similarity 23.0%; Pred. No. 2, 5e-06;

Matches 84; Conservative 56; Mismatches 153; Indels 72; Gaps 17;

QY 87 YDY-ILGRALDALTIPAVGP-----YNRYLTVRSRGCDVLENPISNVDMISAKEK 141

DB 102 YNYTLTRYNATALASPFINDQVKNVDLRYATRPCEMIALIAKTINDSLKELAAAK 161

QY 142 GGPFEASVWFYVIKGDGEDKVC--PIYRKEYRECGDVQLISCAVOSAOMAVDYVPS 199

DB 162 --TYSALRLTWFKIM-----PTCATPIHDVSYMKCNPKLSFAMCDESDILMQASLITM 212

QY 200 TLVSRNGAGLTFSPTAALSGQYLTLTKI-GREAQTALVLEVNDRCKLIGSOLNF-LPS 257

DB 213 AAETDDELGLVLAAPAHASGLYRRIEIDGRIRYTPFSVTIPSERC-PIAFELNENGPD 271

QY 258 KCWTEBOYQTG-----FQGEHLVPIADTNTRHAD-----DYRGEYEDILQRMNLLRK 306

DB 272 RCKTPEOYSRGEVFTRRFELGFENFQGE-----HMTWKFVYVDG-GNLPQVEAQAFA 326

QY 307 NPSAPDRPR--DSVPQELIPAVTKKAEGRTPDAAESSEKKAPPESEDDMQAASGPNP-- 362

DB 327 RVPYRPDHPGFDVSESL-----TQKTKDPKPGQADPKPKNPQPKPKSIK 370

QY 363 -ALPEDDEVPEDETHDDPNSDPDYNDMPAVIPVEETTKSSNAVSMPIFAAFACAVAY 421

DB 371 HLPVRLDEDEVIE-----PYTKPPK--TSSKNSSTFGISVGLGAGLVLV 414

QY 422 GLTWM 426

DB 415 GVILY 419

RESULT 6

VGID_HSVEA

AC P24872: STANDARD; PRT; 402 AA.

DR 01-MAR-1992 (rel. 21, Created)

DR 01-AUG-1992 (rel. 23, Last sequence update)

DR 16-OCT-2001 (rel. 40, Last annotation update)

DE Glycoprotein D precursor (glycoprotein 17/18).

GN GD OR GP17/18 OR 72.

OS Equine herpesvirus type 1 (strain Ab1) (EHV-1).

OC Viruses: dsDNA viruses, no RNA stage: Herpesviridae;

OC Alphaherpesvirinae; Varicellovirus.

OX MBL_TaxID=10328;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=9226882; PubMed=1316942;

RA Elton D.M., Halliburton I.W., Killington R.A., Meredith D.M.,

RA Bonass W.A.,

RT "Identification of the equine herpesvirus type 1 glycoprotein 17/18

RT as a homologue of herpes simplex virus glycoprotein D.";

RL J. Gen. Virol. 73:1227-1233(1992).

LN (2)

RP SEQUENCE OF 242-402 FROM N.A.

RX MEDLINE=91276272; PubMed=1647359;

RA Elton D.M., Halliburton I.W., Killington R.A., Meredith D.M.,

RA Bonass W.A.,

RT "Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine

RT herpesvirus type-1 short unique region.";

RL Gene 101:203-208(1991).

CC -I- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.

CC -----

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CC -----

DR EMBL: M60946; AAA46081.1; -

DR EMBL: M61299; AAA66546.1; -

DR PIR: P00146; P00146.

DR InterPro: IPR002896; Herpes_glycop_D.

DR Pfam: PF01537; Herpes_glycop_D; 1.

DR Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 30 POTENTIAL.

FT CHAIN 1 30 POTENTIAL.

FT DOMAIN 31 402 GLYCOPROTEIN D.

FT TRANSMEM 356 372 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 373 402 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 402 AA; 45211 MW; 78A059323D0238C CRC64;

Query Match 7.6%; Score 175; DB 1; Length 402;

Best Local Similarity 22.6%; Pred. No. 6, 2e-06;

Matches 84; Conservative 53; Mismatches 149; Indels 86; Gaps 17;

QY 87 YDY-ILGRALDALTIPAVGP-----YNRYLTVRSRGCDVLENPISNVDMISAKEK 141

DB 52 YNYTLTRYNATALASPFINDQVKNVDLRYATRPCEMIALIAKTINDSLKELAAAK 111

QY 142 GGPFEASVWFYVIKGDGEDKVC--PIYRKEYRECGDVQLISCAVOSAOMAVDYVPS 199

DB 112 --TYSALRLTWFKIM-----PTCATPIHDVSYMKCNPKLSFAMCDESDILMQASLITM 162

QY 200 TLVSRNGAGLTFSPTAALSGQYLTLTKI-GREAQTALVLEVNDRCKLIGSOLNF-LPS 257

DB 163 AAETDDELGLVLAAPAHASGLYRRIEIDGRIRYTPFSVTIPSERC-PIAFELNENGPD 221

QY 258 KCWTEBOYQTG-----FQGEHLVPIADTNTRHADVRYGEYEDILQRMNLLRK- 305

DB 222 RCKTPEOYSRGEVFTRRFELGFENFQGEHMT-----WLKFFVYVDGGLPQVF 269

QY 306 -----KNPSAPDRPR--DSVPQELIPAVTKKAEGRTPDAAESSEKKAPPESEDDMQAAS 357

DB 270 YEAQAFAPVPPDHPGFDVSESL-----TQKTKDPKPGQADPKPKNPQPKPKSIK 313

QY 358 GENP-----ALPEDDEVPEDETHDDPNSDPDYNDMPAVIPVEETTKSSNAVSMPIFAAFV 414

DB 314 FKWPSIKRLARLDEDEVIE-----PYTKPPK--TSSKNSSTFGISVGLG 357

OY 415 ACAVALVGLWV 426
 Db 358 IAGLVGLVILY 369

RESULT 7

VGDL_HSVB STANDARD; PRT; 452 AA.

AC P24379;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glycoprotein D precursor (Glycoprotein 17/18).
 GN GP17/18 OR 72.
 OS Equine herpesvirus type 1 (strain Ab4p) (EHV-1), and
 OS Equine herpesvirus type 1 (strain Kentucky D) (EHV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicelloviruses.
 NCBI_TaxID=31520, 10330;

SEQUENCE FROM N.A.

STRAIN-AB4P;

RC MEDLINE=92295566; PubMed=1318606;

RA Telford E.A.R., Watson M.S., McBride K., Davison A.J.;

RT "The DNA sequence of equine herpesvirus-1.";

RL Virology 189:304-316(1992).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-Kentucky D;

RX MEDLINE=91108393; PubMed=2177089;

RA Audonnet J.-C., Winslow J., Allen G., Paolletti E.;

RT "Equine herpesvirus type 1 unique short fragment encodes

glycoproteins with homology to herpes simplex virus type 1 gp, gI and

gE.";

RT J. gen. Virol. 71:2969-2978(1990).

RL -1 SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.

CC -1 CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-51 IS THE INITIATOR.

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CC EMBL: M86664; AAC02507.1; -

DR PIR: I36802; VGBEG3.

DR PIR: B36646; VGBEVY.

DR InterPro: IPR002896; Herpes_glycop_D.

DR Pfam: PF01537; Herpes_glycop_D.1.

CC Glycoprotein: Signal; Transmembrane.

FT SIGNAL 1 19 POTENTIAL.

FT CHAIN 20 452 GLYCOPROTEIN D.

FT DOMAIN 20 405 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 406 422 POTENTIAL.

FT DOMAIN 423 452 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 452 AA; 51099 MW; CF51E914F7FE2E9DC CRC64;

SEQUENCE

Query Match 7.6%; Score 175; DB 1; Length 452;
 Best Local Similarity 22.6%; Pred. No. 7.3e-06;
 Matches 84; Conservative 53; Mismatches 149; Indels 86; Gaps 17;

OY 87 YDY-ILGRALDALTTPANGP---YNRYLTRVSRGCVDELNPISNVDMISAAREK 141
 Db 102 YNTIILTRYNATLASPFINDQVKNVDLRIVTATRPCEMIALIAKTINDISILKELAAOK 161
 OY 142 GGFEASVWVFYIKGDGDKYC--PIYKKEVREGCDVLLSECAVQSQMMNAVIVPS 199

Db 162 --TYSARLTWFKIM-----PFCATPIHDVSYKCNPKLSFAMCDBRSIDLMQASLITM 212
 OY 200 TLVSRNGAGLTIESPTALSGQYLLTLKI-GRFAQTALVLEVDRLCKIGSQLN- LPS 257
 Db 213 AAFTEDELGLVLAAPAHASGLYRRVIEIDRRITFDVSVIIPSERC-PIAFEQNFQNP 271
 OY 258 KCMFTEDYQNG-----FQGEHLYPIDNTNRRHADVDYRGEDLILQW-----NLLRK- 305
 Db 272 RCKTPEQYSRGEVTRRLGEFNPQGEHMT-----WLKTFEYDGNLVLQV 319
 OY 306 -----KNPSADDP--DSVPOEIPAVTKKAEGRTPDAESSEKAPPEDESDMQAEAS 357
 Db 320 YEAFAPARVPDPHNPGRDVSSEI-----TQKTPKPKQAPAKPNQ 363
 OY 358 GENPA--ALPEDEVEDTEHDDNSDPDYNDMPAVIYEETKSSNAVSPIFAFAV 414
 Db 364 FKWPSIKHLAPRLDEVEVIE-----PYTKPKK--TSKSNSTFVGISVGLG 407
 OY 415 ACAVALVGLWV 426
 Db 408 IAGLVGLVILY 419

RESULT 8

VGDL_PRIVI STANDARD; PRT; 402 AA.

AC P07645;

DT 01-APR-1988 (Rel. 07, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Glycoprotein GP50.

OS Pseudorabies virus (strain Rice) (PRV).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Varicelloviruses.

NCBI_TaxID=10350;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86281819; PubMed=3016293;

RA Petrovskis E.A., Timmins J.G., Armentrout M.A., Marchloft C.C.,

RA Vancey R.J., Jr., Post L.E.;

RT "RNA sequence of the gene for pseudorabies virus gp50, a glycoprotein

without N-linked glycosylation.";

RL J. Virol. 59:216-223(1986).

RL -1 MISCELLANEOUS: GLYCOPROTEIN GP50 DOES NOT CONTAIN N-LINKED

CARBHYDRATE, AS PREDICTED FROM ITS SEQUENCE.

CC -1 SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.

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CC EMBL: M14001; AAC35203.1; -

DR PIR: A27788; VGBE50.

DR InterPro: IPR002896; Herpes_glycop_D.

DR Pfam: PF01537; Herpes_glycop_D.1.

CC Glycoprotein.

FT SEQUENCE 402 AA; 44501 MW; B876330595871E8 CRC64;

Query Match 7.1%; Score 165; DB 1; Length 402;
 Best Local Similarity 21.0%; Pred. No. 3.5e-05;
 Matches 88; Conservative 55; Mismatches 159; Indels 118; Gaps 19;

OY 73 LLSSEASQSTAAVYDIILG-----RRALDALTTPANGPYRRYLTR-VSRG 117
 Db 6 LLAALVARTLLGADVDAVPAPEPPAYPTESQWLTTLTVSPFVGPADVYHTRPLEDP 65
 OY 118 CDVVELNPISNVDMISAAREKKGFEASVWVFYIKDDGDKCP--IIRKEVREG 175

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Db 66 GCGVALLISDPQVRLNBAVAHRR-PTYRAHVAWYRIADG-----CAHLLEYIEYADC 117
QY 176 GDVQLLSECAVQSAQM---AVDYPSLVSNAGLITFSPALSCQY--LTLTKGR 230
Db 118 DPROVGFGRRTTTPMMTPPSADYFPF---EDELGLMVAHGRNEQYRLVSDGVN 174
QY 231 FAQTLATVLELVNDRCL-KISQSLNLFPSKCMWTEQYOTGQGEHLIPIADNTNRHADY 288
Db 175 ILTFEMVALPFGQECFPFARVDQHRFYKFGACMSDPSFKRGV-----DY 217
QY 289 YR-----GYEDILQRMNNLLRKKN-----PSADPPPSV 319
Db 218 MRFLTFPGQOPRHEVNVW---YRKMKRLLPRAHAATPYADPARPSASGSRPRRP 273
QY 320 QELPAVTKKAGRTPDASSEKKAAPPED-SEDDMQAASGENPALPDEDEVPDETHDD 378
Db 274 RPRPRKPEPAAPAP-----APDRLPPEPATRDHAAGRPFRPRPRPTPH-----R 320
QY 379 PNSDPDYNDMPAYI-----PVEETTKSSNAVS---MPTAAVACAVALLVGLLV 426
Db 321 PFAP-----PAVVPSCWGPQAPAEFPQRTPPAPAGVSRHRSVIVGTGTAMGALLVGVCV 373

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RESULT 9

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ID VGLD_HSV2 STANDARD; PRT; 393 AA.
AC P03172:

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glycoprotein D precursor.
GN OR US6.
OS Herpes simplex virus (type 2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10310;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84131549; PubMed=6321120;
RA Lasky L.A., Dowbenko D.J.;
RT "DNA sequence analysis of the type-common glycoprotein-D genes of
RT herpes simplex virus types 1 and 2."
RT DNA 3:23-29(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84159516; PubMed=6323270;
RA Watson R.J.;
RT "DNA sequence of the Herpes simplex virus type 2 glycoprotein D
RT gene."
RT Gene 26:307-312(1983).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-BKRC;
RA Tertune S.S., Coleman K.T., Sekulovich R., Burke R.L., Spear P.C.;
RT Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
CC 1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GD, GI, AND GE.
CC 1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U12180; AAB60552.1; -
CC EMBL; U12182; AAB60554.1; -
CC EMBL; U12183; AAB60555.1; -
CC EMBL; K02373; AAA45842.1; -
CC EMBL; K01408; AAA45841.1; -

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DR EMBL; AF021342; AAB72102.1; -.
DR PIR; A03731; VGBED2.
DR PIR; A03732; VGBE33.
DR InterPro; IPR002896; Herpes_glycop.D.
DR Pfam; PF01537; Herpes_glycop.D.1.
KW Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 25
FT CHAIN 1 25
FT DOMAIN 26 393
FT TRANSMEM 340 393
FT DOMAIN 364 393
FT CARBOHYD 119 119
FT CARBOHYD 146 146
FT CARBOHYD 287 287
FT VARIANT 249 249
FT VARIANT 337 337
FT VARIANT 367 369
SQ SEQUENCE 393 AA; 43147 MW; A8514E21857AEDF2 CRC64;

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Query Match 6.8%; Score 156.5; DB 1; Length 393;
Best Local Similarity 21.0%; Pred. No. 0.00015;
Matches 59; Conservative 50; Mismatches 137; Indels 35; Gaps 8;

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QY 97 DALTPAVGEYKXLYLTRVSGCDVLENPISNVDMSIAKKEKGFPEASVWFYIK 156
Db 71 DFPQPSI-PIFYVAVLERACRSVLLHAPSEAPQIVRGSADPAKRTNLTITARM-- 127
QY 157 GDGGEKCYPIYKEKEKRGCDVQLSECAVQSAQMADVSTLVSRNAGLITFSPTA 216
Db 128 ---GDGCAIPFYMEYTEEDPYKSLGVCIPRQPSY-YDFSAVSEEDNLCFLHAPAF 183
QY 217 ALSGOYLTLKIGRFAQTLATVLEVNDRC-LKISQSLNLFPSKCMWTEQYOTGQGEHLIY 275
Db 184 ENAGTYLRVKNIDMETIQLFLEHRAKSCYALPLRPPACLTSAKYQGVTVDSIG 243
QY 276 PIADNTNRHADVVRGEDIQRMNNLLRKNPSADPRP---DSVQELPAVTKKAAG 331
Db 244 MLEPTPEN-----QRTVALYSLKTAGHNGKPRPYSLLPPELSDT----- 286
QY 332 RPPDAESSEKKAAPPEDSED-MQAEASGENPALPDEDEVP 371
Db 287 -----NATQPELVPEDEPDSALLEDPAGVSSQIPPMHHP 322

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RESULT 10

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ID VGLD_HSVBP STANDARD; PRT; 417 AA.
AC P24906:

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DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glycoprotein D precursor (Glycoprotein IV).
GN GD OR GIV OR US6.
OS Bovine herpesvirus type 1 (strain p8-2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10324;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 19-48.
RX MEDLINE=90376470; PubMed=2168991;
RA Tikoo S.K., Fitzpatrick D.R., Babiuk L.A., Zamb T.J.;
RT "Molecular cloning, sequencing, and expression of functional bovine
RT herpesvirus 1 glycoprotein gIV in transfected bovine cells."
RT J. Virol. 64:5132-5142(1990).
CC 1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.

```

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CC use by non-profit institutions as long as its content is in no way
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DR EMBL: Z23068; CAAB0604.1; -
 DR InterPro: IPR002896; Herpes_glycop_D.
 DR Pfam: PF01537; Herpes_glycop_D.1.
 KW Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 417 BY SIMILARITY.
 FT DOMAIN 19 360 GLYCOPROTEIN D.
 FT TRANSMEM 361 389 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 390 417 POTENTIAL.
 FT CARBOHYD 41 41 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 417 AA; 45020 MW; 82E1E875BF2DF9C CRC64;

Query Match 6.0%; Score 139.5; DB 1; Length 417;
 Best Local Similarity 22.2%; Pred. No. 0.003;
 Matches 88; Conservative 41; Mismatches 179; Indels 89; Gaps 16;

OY 58 MDRLFLRNAFWTIVLLSSFASQSTAAVYDITLGRRLDALTIPAGVRYRLTRVSRG 117
 DB 37 MFRVYTERMTTGPISPPADGREGQVENVRAASAAACMLALADPOVGRITMEAVR- 95
 OY 118 CDVVELNPISNVDDMISAKKEKGGPEASVWVYIKGDGEDKYC--PIYREKREC 175
 DB 96 -----RHAAYNATVYWKIESG-----CARPLYMETEC 126
 OY 176 GDVOLLSECAVSAQMAVDPVPTLVSRNGAGLTIPSPTAALSGOYLLTKI-GRPAOT 234
 DB 127 EPRKHFGYCRRTPEFMDSLAGFAYPTDDELGLMAAPARLVGOYRFAIYIDGTVAYT 186
 OY 235 -ALVTELVNDRCLKIGSOLNPLPSKQWTEYOYQTFQGEHL-----YR-----I 277
 DB 187 DFMWLPAGD-CMFPSKIDPARGYTFSAQCFARERE--QNVVLTLTYLTQYPOEAKAI 242
 OY 278 AD-INTRHADV-----YGEYEDILORNNLTKKNSAPDRPDSVPOETPAVTKAE 330
 DB 243 VDYMFRHGGVPPYFEESKGYE-----PPPAAGD---GSPAPPCDDE 282
 OY 331 GRTDASSEKKAPPESEDMDQAEASGENPALPEDEVEDTEHDDPSDDPYNDMP 390
 DB 283 AREDEGETEDGAGRENGGPRGPEGESPT--PEANGAGEBPKRPSPADRPREGWP 340
 OY 391 AV-----IPEETTKSSNAVSMPIFAAFVACAVALV 421
 DB 341 SLEATTPPPAPATPAPADAVPVGVGIGIAAIAICV 377

RESULT 13
 VGX PRIVI STANDARD: PRT; 498 AA.
 AC P07362;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Secreted glycoprotein Gx.
 GN Gx.
 OS Pseudorabies virus (strain Rice) (PRV).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicelloviruses.
 OX NCBI_TaxID=10350;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85135070; PubMed=2983115;
 RA Rea T.J., Timmins J.G., Long G.W., Post L.E.;
 RT "Mapping and sequence of the gene for the pseudorabies virus
 glycoprotein which accumulates in the medium of infected cells.";
 RL J. Virol. 54:21-29(1985).
 CC - SIMILARITY: TO EBV-1 GLYCOPROTEIN G.
 CC -----

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DR EMBL: M10986; AAC35206.1; -
 DR PIR: A21879; VGBEGX.
 DR InterPro: IPR003363; Herpes-gc.
 DR Pfam: PF02400; Herpes-gc.1.
 KW Glycoprotein.
 FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 498 AA; 53721 MW; 17DA180672A6ZDD CRC64;

Query Match 5.6%; Score 129; DB 1; Length 498;
 Best Local Similarity 23.5%; Pred. No. 0.024;
 Matches 73; Conservative 32; Mismatches 115; Indels 90; Gaps 13;

OY 95 ALDALTPAYGPNRYLTRYSGCDVLENPISVNDMISAKKEKGGPEASVWVYV 154
 DB 43 ATDAQPVNPLAPANATGTDYSKCEMKLLDPLDVSSRSS-----DPVNTVAMFP- 93
 OY 155 IKGDGEDKXCPYRREYREC-GD-----VOLSECAVSAQMAVDP 195
 DB 94 ----DGCHCKVPLVHREYVGGCPDAMPVETCGYSTRTTRIDTLMETALVNASL----- 145
 OY 196 YVSTLVSRNGAGLTIPSPTAALSGOYLLTKIGRPAQALVTELVNDRCLKIGSOLNPL 255
 DB 146 -----VLQGLYDAGLYIVLVFGDPAVIGVLSVEAN-----L 180
 OY 256 PSKQWTEYOYQTFQGEHLYPIADTNTRHADVYRGEYEDILORNNLTKKNSAPDRP 315
 DB 181 DYPCKMKHGLITTRPATITPPIAFTAGDH-----QRMKRCF-----PST 219
 OY 316 DSVPOETPAVTKAEGRPD-AESEKKAPPESEDMDQAEASGENPALPEDEVEDTEH 374
 DB 220 DEGAME--NVTAAEKGLSDYADYDVHIFRSESDV-----VHGAPRA-PGEVYTEE- 272
 OY 375 EHDDEPSDDP 384
 DB 273 EAEITSSDLD 282

RESULT 14
 GAK HUMAN STANDARD: PRT; 1311 AA.
 AC O14976; Q9BYV6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cyclin G-associated kinase (EC 2.7.1.1-).
 GN GAK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC TISSUE=Fibroblast;
 RX MEDLINE=97446136; PubMed=9299234;
 RA Kinura S.H., Tsutuga H., Yabuta N., Endo Y., Nojima H.;
 RT "Structure, expression, and chromosomal localization of human GAK.";
 RL Genomics 44:179-187(1997).
 RN [2]
 RP SEQUENCE OF 981-1311 FROM N.A.
 RC TISSUE=Placenta;
 RA Strausberg R.;
 RN Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC [3]
 CC FUNCTION, AND SUBCELLULAR LOCATION.
 RX MEDLINE=20092914; PubMed=10625686;
 RA Greener T., Zhao X., Nojima H., Eisenberg E., Greene L.E.;

RT "Role of cyclin G-associated kinase in uncoating clathrin-coated vesicles from non-neuronal cells";
 RL J. Biol. Chem. 275:1365-1370(2000).
 CC -1- FUNCTION: Associates with cyclin G and CDK5. Seems to act as an axillin homolog that is involved in the uncoating of clathrin-coated vesicles by Hsc70 in non-neuronal cells. Expression oscillates slightly during the cell cycle, peaking at G1.
 CC -1- SUBCELLULAR LOCATION: Localizes to the perinuclear area and to the trans-Golgi network. Also seen on the plasma membrane, probably at focal adhesions.
 CC -1- TISSUE SPECIFICITY: Ubiquitous. Highest in testis.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 1 TENSIN DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 J DOMAIN.
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 CC -----
 DR EMBL; D88435; BAA22623.1; -
 DR EMBL; BC000816; AAH00816.1; -
 DR EMBL; BC008668; AAH08668.1; -
 DR Genew; HGNC:4113; GAK.
 DR MIM; 602052; -
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR000719; Euk_Pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_Pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00228; DnaJ; 1.
 DR ProDom; PD000001; Euk_Pkinase; 1.
 DR SMART; SM00271; DnaJ; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00219; TYRKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00636; DnaJ_1; FALSE_NEG.
 DR PROSITE; PS00076; DnaJ_2; 1.
 KM Transferrase: Serine/threonine-protein kinase; ATP-binding;
 KW Nuclear protein; Endoplasmic reticulum; Cell cycle.
 FT DOMAIN 40 314
 FT ACT_SITE 173 173 BY SIMILARITY.
 FT DOMAIN 347 350 POLY-PRO.
 FT DOMAIN 407 691 TENSIN.
 FT DOMAIN 1247 1311 J-DOMAIN.
 FT CONFLICT 1113 1113 P -> A (IN REF. 1).
 SQ SEQUENCE 1311 AA; 143190 MW; 0ACE45DF57A5F981 CRC64;
 Query Match 5.1%; Score 118.5; DB 1; Length 1311;
 Best Local Similarity 19.5%; Pred. No. 0.54;
 Matches 96; Conservative 74; Mismatches 144; Indels 179; Gaps 28;
 QY 4 PHLRHSYTYAKGEVNLKMDCG--GKRCGSAVFTLFMTG-----VIRMEHICVR 55
 DB 457 PRTYRPSRFH-----NRVSECGMAARR--APHLHTLYNCRNMHAWLRDQHKVVCV- 506
 QY 56 NAMRHLFLNAFWTIVLLSFASSOSTAAVYDILGRALDALTIPIVGP-YNYRLRV 114
 DB 507 HCMGGRASAVAVCSFLCFRLESTAEAAV-YFMSKR-----CPPEIWSHKRYIYWM 559
 QY 115 SRGCDVVLNFIISVNDMISAKKEKGKGFVAVVYVY-----KSDGDEKXCP 166
 DB 560 ---CDMAEERIT-----PHSKPIIVRAVYVMTVPVPLFSKQSRGCRPCE 600
 QY 167 IY-----RKETRECGDVQLISECAVQSAQMMADVDPSTLVSRNGAGLTIPSPAA 217
 DB 601 VYVDDEKVASTQSTQYDKMRDKIEDGKAV-----IPLGTVAGQDVLIVYHARST 650

QY 218 LSGGVLTLLTKIGFAQTALVLTLEVNDROLKIGSOLNPLPSKOWTTE--QYOTGFGGHLV 275
 DB 651 LGGR-----LQAKKASMKM-----FQJOPHTGFVPRNATYKFAKTYD----- 688
 QY 276 PIADNTNRHADDVYRGVEDILO-----RW-NNLLRRKN-----SAPD 312
 DB 689 -----DADQIQKRYDLPQVNLVEVEPRDRSREAPWENSMTGLNPKILFSSRE 740
 QY 313 PRPD-----SVQELIPAVTKK--AGCRIPDAESSEKKAPDESD-----DMQA 354
 DB 741 EOODILSKFGKRELPRQ-PGSTAQYDAGASPEAPEPTSDSPSSSADASRLHTLDQOE 799
 QY 355 E-----ASGENPALPED-----DE--VPEDTEHDDPNDDP----- 384
 DB 800 EKEATGAEINSSKSESALMEDRDESEVSDGGSFISSEGOEPRADPEPELANGLVQO 859
 QY 385 ---YYNDMPAVIP 394
 DB 860 DLVFEVETPAVLIP 872
 RESULT 15
 XPR6_YARLI STANDARD: PRT: 976 AA.
 ID XPR6_YARLI
 AC P42781.
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Dibaasic processing endoprotease precursor (EC 3.4.21.-).
 GN XPR6.
 OS Yarrowia lipolytica (Candida lipolytica).
 CC Eukaryote; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Dipodascaceae; Yarrowia.
 OX NCBI_TaxID:4952;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CX-161-1B;
 RX MEDLIND=94262316; Pubmed=8203153;
 RA Enderlin C.S., Ogrzydzik D.M.,
 RT "Cloning, nucleotide sequence and functions of xpr6, which codes for a dibasic processing endoprotease from the yeast Yarrowia lipolytica";
 RT 1 lipolytica";
 RL Yeast 10:67-79(1994).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8. PURIN SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; L16238; AAA20573.1; -
 DR HSSP; O45670; IDBI.
 DR MEROPS; S08.070; -
 DR InterPro; IPR002884; P_domain.
 DR InterPro; IPR000209; Peptidase_S8.
 DR Pfam; PF01483; P; PARTIAL.
 DR PRINTS; PRO0723; SUBTILISIN.
 DR ProDom; PD000717; P_domain; 1.
 DR PROSITE; PS00136; SUBTILASE_ASP; 1.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; 1.
 KM Hydrolyase; Serine protease; Glycoprotein; Calcium; Transmembrane;
 KW Zymogen; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 976 POTENTIAL.
 FT DOMAIN 211 230 DIBASIC PROCESSING ENDOPROTEASE.
 FT TRANSMEM 524 544 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT TRANSMEM 855 875 POTENTIAL.
 FT ACT_SITE 311 311 POTENTIAL.
 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT ACT SITE 349 349 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 528 528 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 886 886 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 976 AA; 110024 MW; 038C5999E7E8F6F6 CRC64;

Query Match 5.0%; Score 116; DB 1; Length 976;
Best Local Similarity 23.9%; Pred. No. 0.56; Indels 40; Gaps 8;

Matches 57; Conservative 31; Mismatches 110; Indels 40; Gaps 8;

QY 216 AALSGOYLITKIGRFAQTALVTLFVNDRLKIGSQLNLPKSCWTEQYQTFQGEHLX 275
Db 657 ASYRGHVRLKGRGVVSELAALRRDRSKDGYNNMAFMVAHWAD-----GGGDW 709
QY 276 PIADTNTKHA-----DYRYGEDILQRMNNLLRKNPSADPPRDSVPOEIPAVT 326
Db 710 ELTVNTGEQDOVELVNMQLNVFGEQKD--KREKREGESKRPEDENKGEKEGKRPED 767
QY 327 KKAEGRTPDASESEKKAPDESEDMDQAEASGENPALPED--DEVPEDEHDPNSDPD 384
Db 768 NKEGKEDDKGDKEDKEDKEDKEDKEDKEDKEDKEDKEDKEDKEDKEDKEDKEDKED 818
QY 385 YNDMPAVIPEVETKSSNAVSMPI-----AAEVACAVALVG--LLVWSIVKC 431
Db 819 KPEKPEKPYDNDSSSDSSDSSHTSWMPDLSKRSAMLYGAVLLVGFTAVIGIYAC 876

Search completed: February 19, 2003, 16:21:35
Job time : 16 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2003, 16:21:11 ; Search time 35 Seconds
(without alignments)
2534.984 Million cell updates/sec

Title: US-09-994-064-11

Perfect score: 2311
Sequence: 1 MHRPHLRHSRYAKGEVLN.....ACAVALVGLLWSIVACARS 434

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2311	100.0	434	12	067644 gallid herp
2	1860	80.5	371	12	069294 gallid herp
3	190	8.2	394	12	069082 human herpe
4	190	8.2	394	12	069081 human herpe
5	190	8.2	394	12	005059 human herpe
6	190	8.2	394	12	005060 human herpe
7	188	8.1	394	12	080RB6 human herpe
8	186.5	8.1	394	12	0991M3 human herpe
9	184	8.0	394	12	091NH6 human herpe
10	180	7.8	384	12	080RB7 human herpe
11	175	7.6	402	12	004245 equine herp
12	169	7.3	400	12	091W02 pseudorabie
13	169	7.3	516	12	091W00 pseudorabie
14	162.5	7.0	374	12	089634 feline herp
15	162	7.0	398	12	09YS31 pseudorabie
16	159	6.9	404	12	092290 pseudorabie

17	159	6.9	417	12	065535 bovine herp
18	158	6.8	393	12	069467 herpes simp
19	151.5	6.6	403	12	067648 turkey herp
20	151.5	6.6	403	12	096616 turkey herp
21	146	6.3	402	12	039308 equine herp
22	146	6.3	402	12	086652 equine herp
23	141.5	6.1	403	12	069286 turkey herp
24	135.5	5.9	395	12	069369 cercopithe
25	134	5.8	385	12	098939 gallid herp
26	134	5.8	385	12	012378 melegriid h
27	131.5	5.7	384	12	09DP33 turkey herp
28	131.5	5.7	384	12	088523 turkey herp
29	129	5.6	499	12	0913H9 pseudorabie
30	125	5.4	345	12	041524 canine herp
31	124.5	5.4	394	12	08V2D6 simlan herp
32	124.5	5.4	394	12	08V2D5 simlan herp
33	124.5	5.4	394	12	08UYJ1 simlan herp
34	124.5	5.4	394	12	08UYA3 simlan herp
35	124.5	5.4	394	12	08UYA2 simlan herp
36	123.5	5.3	237	12	041201 pseudorabie
37	122.5	5.3	384	12	08V2D4 simlan herp
38	121.5	5.3	394	12	08UYF8 simlan herp
39	120	5.2	394	12	08V2D3 simlan herp
40	117	5.1	303	10	09M4U5 O9m4us zea mays (m
41	115.5	5.0	614	5	094674 plasmodium
42	115	5.0	394	12	08V724 simlan herp
43	115	5.0	1648	11	09Q205 mus musculu
44	114	4.9	1370	11	09ESB8 mus musculu
45	114	4.9	1570	11	09ESB6 mus musculu

ALIGNMENTS

RESULT 1

067644 PRELIMINARY: PRT: 434 AA.
AC 067644;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Glycoprotein D.
OS Gallid herpesvirus 1
OC viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.
OX NCBI_TaxID=10386;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-USDA CHALLENGE STRAIN:
RX MEDLINE=97033380; PubMed=8879127;
RA Wild M.A., Cook S., Cochran M.;
RT "A genomic map of infectious laryngotracheitis virus and the sequence
RT and organization of genes present in the unique short and flanking
RT regions";
RU Virus Genes 12:107-116(1996).
DR EMBL: U28832; AAC5100.1; -.
DR Interpro: IPR002896; Herpes_glycop.D.
DR Pfam: PF01537; Herpes_glycop.D; 1.
SQ SEQUENCE 434 AA: 48472 MW: 792A34D52675F52 CRC64;

Query Match 100.0%; Score 2311; DB 12; Length 434;
Best Local Similarity 100.0%; Pred. No. 6; 1e-185;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRPHLRHSRYAKGEVLNHHDCGKRCSCGAATFTFWTCVRIHREHICFRNAMD 60
Db 1 MHRPHLRHSRYAKGEVLNHHDCGKRCSCGAATFTFWTCVRIHREHICFRNAMD 60
QY 61 HLFRLNFWTIVLLSFAASSTAAVTYDITIGRRALDALTPAVGPYRNLTRYSGCDV 120
Db 61 HLFRLNFWTIVLLSFAASSTAAVTYDITIGRRALDALTPAVGPYRNLTRYSGCDV 120
QY 121 VELNPISNVDMISAAKEKEGPFEEASVYWFYIKGDDEDKTCPIYRKREYECGDVQL 180

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Db 121 VELNFSNVDDMISAAK EKEGKGPPEASVWFYVTKGDGDEKCPYIRKREYREGQVQL 180
Qy 181 LSECAVQSAQMAVADVSTLVSRNGAGLTTFSPALSGOYLTLTKGPAQALVYLE 240
Db 181 LSECAVQSAQMAVADVSTLVSRNGAGLTTFSPALSGOYLTLTKGPAQALVYLE 240
Qy 241 VNRCLKIGSOLNPLPSKCMTEQYOTGFOGHEHLYPIADTNTNRHADVDYRGEDILQ 300
Db 241 VNRCLKIGSOLNPLPSKCMTEQYOTGFOGHEHLYPIADTNTNRHADVDYRGEDILQ 300
Qy 301 NLKKKNSAPDPDPDSYPOEIPAVTKKAGRTDPAESSEKKAPPEDEDDMQAASGEN 360
Db 301 NLKKKNSAPDPDPDSYPOEIPAVTKKAGRTDPAESSEKKAPPEDEDDMQAASGEN 360
Qy 361 PALPPEDEVEDETHDDPNSDPDYNDMPAVIPEETTTSSNANSPRIFAAPACAVAL 420
Db 361 PALPPEDEVEDETHDDPNSDPDYNDMPAVIPEETTTSSNANSPRIFAAPACAVAL 420
Qy 421 VGLLWMSIVKCAR 434
Db 421 VGLLWMSIVKCAR 434

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RESULT 2

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ID 069294 PRELIMINARY; PRT; 371 AA.
AC 069294;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, last annotation update)
DE Glycoprotein D.
GN GD
OS Gallid herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.
OX NCBI_TaxID=10386;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SA-2;
RX MEDLINE=95337426; PubMed-7612933;
RA Johnson M.A., Tyack S.G., Prideaux C.T., Kongsuwan K., Sheppard M.;
RT "Sequence characteristics of a gene in infectious laryngotracheitis
RT virus homologous to glycoprotein D of herpes simplex virus."
RL DNA Seq. 5:191-194(1995).
DR EMBL: L31965; AAA89825.1;
DR InterPro: IPR002896; Herpes_glycop_D.
DR Pfam: PF01537; Herpes_glycop_D.1.
SQ SEQUENCE 371 AA; 41229 MW; AE81A493112A4489 CRC64;

```

Query Match

Best Local Similarity 80.5%; Score 1860; DB 12; Length 371;

Matches 355; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```

Qy 58 MDRHLFLRNAFTYVILSSFSASOSTAAVYDYILGRALDALTPAVGPNRYLTVRSNG 117
Db 1 MDRHLFLRNAFTYVILSSFSASOSTAAVYDYILGRALDALTPAVGPNRYLTVRSNG 60
Qy 118 GCVLELNPISNVDDMISAKEKEGPFASVWFYVTKGDGDEKCPYIRKREYREGCD 177
Db 61 GCVLELNPISNVDDMISAKEKEGPFASVWFYVTKGDGDEKCPYIRKREYREGCD 120
Qy 178 VOLTSECAVQSAQMAVADVSTLVSRNGAGLTTFSPALSGOYLTLTKGPAQALVYLE 237
Db 121 VOLTSECAVQSAQMAVADVSTLVSRNGAGLTTFSPALSGOYLTLTKGPAQALVYLE 180
Qy 238 TLEVNDRLKIGSOLNPLPSKCMTEQYOTGFOGHEHLYPIADTNTNRHADVDYRGEDILQ 297
Db 181 TLEVNDRLKIGSOLNPLPSKCMTEQYOTGFOGHEHLYPIADTNTNRHADVDYRGEDILQ 240
Qy 298 RWNLLRKKNSAPDPDPDSYPOEIPAVTKKAGRTDPAESSEKKAPPEDEDDMQAAS 357
Db 241 RWNLLRKKNSAPDPDPDSYPOEIPAVTKKAGRTDPAESSEKKAPPEDEDDMQAAS 300

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Qy 358 GENPALPEDEVEDETHDDPNSDPDYNDMPAVIPEETTTSSNANSPRIFAAPACAV 417
Db 301 GENPALPEDEVEDETHDDPNSDPDYNDMPAVIPEETTTSSNANSPRIFAAPACAV 360
Qy 418 VALVG 422
Db 361 VALVG 365

```

RESULT 3

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ID 069082 PRELIMINARY; PRT; 394 AA.
AC 069082;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE Glycoprotein D precursor.
OS human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94160582; PubMed-8116256;
RA Dean H.J., Terhune S.S., Shieh M.T., Spear P.G.;
RT "Single amino acid substitutions in glycoprotein D of herpes simplex
RT virus type 1 that confer resistance to gd-mediated interference also
RT alter virus infectivity."
RL Virology 199:67-80(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Dean H.J., Terhune S.S., Johnson R.M., Spear P.G.;
RT "Variability among strains of Herpes simplex virus in sensitivity to
RT gd-mediated interference."
RT Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
RL EMBL: L09244; AAA19631.1;
DR InterPro: IPR002896; Herpes_glycop_D.
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF01537; Herpes_glycop_D.1.
DR PROSITE: PS00266; SOMATOTROPIN_1; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 25
FT CHAIN 26 394
FT VARIANT 52 52 R -> Q (IN REF. 2).
FT SEQUENCE 394 AA; 43344 MW; 1076f2f0c8a1d73b CRC64;

```

Query Match

Best Local Similarity 8.2%; Score 190; DB 12; Length 394;

Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

```

Qy 106 PYNRLTVRSNGCDVLELNPISNVDDMISAKEKEGPFASVWFYVTKGDGDEKCPY 165
Db 79 PITYYAVLNRACNSVILNAPSEAPQYRGASEVYKOPVULTAPFRM-----GGNCAL 133
Qy 166 PYYRKEVEGCDVOLLSECAVQSAQMAVADVPS-TLVSRNGAGLTTFSPALSGOYL 224
Db 134 PITYWEYTECSYNSLGCPIRTQPRW--NYDSEFSAVSEDNGLFMAHAFETAGTYLR 191
Qy 225 TLKIGRPAQALVYLE--VNRCLKIGSOLNPLPSKCMTEQYOTG-----FOG 271
Db 192 LVKINDWELTQFLIEHRKAGC-KYALPLRTPSPASLSPAYOQGYTVDSIGMLPRFIP 250
Qy 272 EHLVPIADTNTNRHADVDYRGEDILQWNNLLRKKNSAPDPDPDSYPOEIPAVTKKAG 331
Db 251 ENQRTAVAVYSLKIG-----WH-----GFKAP-YTSTLTPPEL-----S 283
Qy 332 RTPAESSEKKAPPEDEDD-MQAASGENPALPEDEVEDETHDDPNSDPDYNDMP 390
Db 284 ETPNA--TOPELAPPEDEDSALLEDPVGTVAQIPRWGHTPSQDADATGYHPRATRNNG 341
Qy 391 AVIPEETTTSSNANSPRIFAAPACAVVALVGLIV 426

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Db 342 LI-----AGAVGSLAALVYC-----GIYWM 363

RESULT 4

ID Q06081 PRELIMINARY; PRT; 394 AA.

AC Q06081;

DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE Glycoprotein D precursor.

OS human herpesvirus 1.

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Simplexvirus.

NCBI_TaxID=10298;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94160582; PubMed=8116256;

RA Dean H.J., Terhune S.S., Shieh M.T., Spear P.G.;

RT "Single amino acid substitutions in glycoprotein D of herpes simplex virus type 1 that confer resistance to gp-mediated interference also

RT alter virus infectivity."

RL Virology 199;67-80(1994).

RN [2]

RP SEQUENCE FROM N.A.

RA Dean H.J., Terhune S.S., Johnson R.M., Spear P.G.;

RT "Variability among strains of Herpes simplex virus in sensitivity to

RT gp-mediated interference."

RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.

DR EMBL; L09245; AAA19630.1; -.

DR InterPro; IPR002896; Herpes_glycop_D.

DR InterPro; IPR001400; Somatotropin.

DR Pfam; PF01537; Herpes_glycop_D.1.

DR PROSITE; PS00266; SOMATOTROPIN_1; UNKNOWN_1.

KW Signal.

FT SIGNAL

FT CHAIN

FT VARIANT

SQ SEQUENCE

394 AA; 43285 MW; 7FBEB5A1E8FDC0BF CRC64;

Query Match

Best Local Similarity 8.2%; Score 190; DB 12; Length 394;

Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

Db 106

PYNKYLIRVSGCDVNLNPSNVDMISAKEKEGPREASVWVYVYKGDGDEKVC

PITVYVAVLERACRSVLLNAPSEAPQIVRGASEDVRRQPNVLTAMFRM-----GGCAI

PIYRKEYREGCDVOLLSECAVQSAQMAVADVPS-TLVSRNGAGLTIESPTAALSGOYL

PITVMEETECYSKSLGACPIRTQPRM--NYDSFSAVSEDNLGFLMHARAFETAGTYLR

TLKIGRFAQTALVLE--VNDRLKIGSQNLFLPSKCTTEQYOTG-----FOG

LVKINDTEITQFLIEHRAKGC-KYALPLRIPSACTSPQAYQOGVTVDISIGMLPRFIP

EHLPIADTNRHADVDYRGEDILQRMNNLKRKNSADPRDSYQOEIPANTKKAEG

ENORTTAVVSLIKTAG-----WH-----GPKAP-YTSTLLPRPL-----S

RTDPAESSEKAPPEDESD-MQAEASGENPALPPEDEVEDTEHDHPSPDPDYNDMP

ETRNA--TOPELAPDEDESDALLEDPYGTVAPQIRPMWHIPSIQDATAATYRHNPRATRNMG

AVIPVEETTKSSNAVSPRIFAAYACAVVALVGLIWM

LI-----AGAVGSLAALVYC-----GIYWM

342

394 AA.

PRELIMINARY;

PRT;

394 AA.

005059;

005059;

005059;

005059;

005059;

005059;

005059;

005059;

005059;

005059;

005059;

005059;

DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)

DE Glycoprotein D precursor.

OS human herpesvirus 1.

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Simplexvirus.

NCBI_TaxID=10298;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=E;

RA MEDLINE=94160582; PubMed=8116256;

RX Dean H.J., Terhune S.S., Shieh M.T., Spear P.G.;

RT "Single amino acid substitutions in gp of herpes simplex virus 1

RT confer resistance to gp-mediated interference and cause cell-type-

RT dependent alterations in infectivity."

RL Virology 199;67-80(1994).

CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,

CC GB, GC, GG, GD, GI, AND GE.

CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN D.

DR EMBL; L09242; AAB59754.1; -.

DR InterPro; IPR002896; Herpes_glycop_D.

DR InterPro; IPR001400; Somatotropin.

DR Pfam; PF01537; Herpes_glycop_D.1.

DR PROSITE; PS00266; SOMATOTROPIN_1; UNKNOWN_1.

KW Glycoprotein; Transmembrane; Signal.

FT SIGNAL

FT CHAIN

FT DOMAIN

FT TRANSMEM

FT DOMAIN

CARBOHYD

CARBOHYD

CARBOHYD

SEQUENCE

394 AA; 43307 MW; 90593FC19486AC5 CRC64;

Query Match

Best Local Similarity 8.2%; Score 190; DB 12; Length 394;

Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

Db 106

PYNKYLIRVSGCDVNLNPSNVDMISAKEKEGPREASVWVYVYKGDGDEKVC

PITVYVAVLERACRSVLLNAPSEAPQIVRGASEDVRRQPNVLTAMFRM-----GGCAI

PIYRKEYREGCDVOLLSECAVQSAQMAVADVPS-TLVSRNGAGLTIESPTAALSGOYL

PITVMEETECYSKSLGACPIRTQPRM--NYDSFSAVSEDNLGFLMHARAFETAGTYLR

TLKIGRFAQTALVLE--VNDRLKIGSQNLFLPSKCTTEQYOTG-----FOG

LVKINDTEITQFLIEHRAKGC-KYALPLRIPSACTSPQAYQOGVTVDISIGMLPRFIP

EHLPIADTNRHADVDYRGEDILQRMNNLKRKNSADPRDSYQOEIPANTKKAEG

ENORTTAVVSLIKTAG-----WH-----GPKAP-YTSTLLPRPL-----S

RTDPAESSEKAPPEDESD-MQAEASGENPALPPEDEVEDTEHDHPSPDPDYNDMP

ETRNA--TOPELAPDEDESDALLEDPYGTVAPQIRPMWHIPSIQDATAATYRHNPRATRNMG

AVIPVEETTKSSNAVSPRIFAAYACAVVALVGLIWM

LI-----AGAVGSLAALVYC-----GIYWM

342

394 AA.

PRELIMINARY;

PRT;

394 AA.

005060;

005060;

005060;

005060;

005060;

005060;

005060;

005060;

005060;

005060;

005060;

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DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE Glycoprotein D precursor.
OS human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CX Alphaherpesvirinae; Simplexvirus.
RN NCBI_TaxID=10298;
RP SEQUENCE FROM N.A.
RA MEDLINE=94160582; PubMed=8116256;
RT Dean H.J., Terhune S.S., Shieh M.T., Spear P.G.;
RT "Single amino acid substitutions in gd of herpes simplex virus 1
RT confer resistance to gp-mediated interference and cause cell-type-
RT dependent alterations in infectivity.";
RL Virology 199;67:80(1994).
CC -1 MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1. GH,
CC GH, GC, GG, GD, GI, AND GE.
CC -1 SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN D.
DR EMBL; L09243; AAA19629.1; -.
DR InterPro; IPR002896; Herpes-glycop_D.
DR Pfam; PF01537; Herpes-glycop_D; 1.
DR PROSITE; PS00266; SOMATOTROPIN_1; UNKNOWN_1.
KW Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 25
FT CHAIN 26 394 GLYCOPROTEIN D.
FT DOMAIN 26 339 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 340 364 POTENTIAL.
FT DOMAIN 365 381 STRONGLY BASIC REGION;
FT WHICH PROBABLY SERVES TO ANCHOR THE
FT GLYCOPROTEIN IN THE MEMBRANE.
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 394 AA; 43316 MW; 90540F0F1953CB7F CRC64;

Query Match 8.2%; Score 190; DB 12; Length 394;
Best Local Similarity 23.2%; Pred. No. 1.3e-07;
Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

DY 106 PYNRYLTVSRGCDVVELNPISNVDNMISAKEKEGPFESVWFYIKGDDGEDKYC 165
DB 79 PIVVYAVLERACRSVLNAPSEAPQIVRGASEDVAKOPYNLTIAFRM-----GNCAL 133
QY 166 PIYKREYREGDVQLISECAVSAQMMAVDYPS-TLVSRNGAGLTIFSTALSGQYL 224
DB 134 PIVMEYTCYSYKKSIGACPIRTQPRW--NYDSFSAVSEDLGFLMHAPEETAGTYLR 191
QY 225 TLKIGRFQALVTL--VNDRCIKIGSQLNLPSCWTTEDYQTG-----FOG 271
DB 192 LVKINDMTETITQFLIHRKAGSC-KYALPLRIPPSACLSPOAYQGVVDSIGMLPRFIT 250
QY 272 EHLYPADINTRHADVYNGYEDILQRMNNLLRKNPSAPDRPDSVQOEIPAVTKKAG 331
DB 251 ENQRTVAVYSLKLAG-----WH-----GPKAP-YTSTLLPEL-----S 283
QY 332 RPPDAESSEKKAPEDESD-MQAEASGENPALPEDEDETHDPSNDPYYNDMP 390
DB 284 ETPNA--TQPELAPDEPDESALLEDPVGVAPQIPPMHIFSIQDAAPFHPAPPPNMG 341
QY 391 AVIPEETTKSSNAVSMPIFAFVACAVALVGLTW 426
DB 342 LI-----AGAVGGSILALALVIC-----GIYVW 363

RESULT 7
OQORB6 PRELIMINARY; PRT; 394 AA.
AC OQORB6;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Glycoprotein D.
OS human herpesvirus 1.

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OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CX Alphaherpesvirinae; Simplexvirus.
RN NCBI_TaxID=10298;
RP SEQUENCE FROM N.A.
RA Kim J.K., Kim Y.K., Hong J.B., Kim S.Y., Ahn J.K.;
RT "Isolation of the enhanced neurovirulent HSV-1 strains from Korean
RT patients.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF487902; AAL90884.1; -.
SQ SEQUENCE 394 AA; 43286 MW; 8750DAC984CDS25D CRC64;

Query Match 8.1%; Score 188; DB 12; Length 394;
Best Local Similarity 23.2%; Pred. No. 1.8e-07;
Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

DY 106 PYNRYLTVSRGCDVVELNPISNVDNMISAKEKEGPFESVWFYIKGDDGEDKYC 165
DB 79 PIVVYAVLERACRSVLNAPSEAPQIVRGASEDVAKOPYNLTIAFRM-----GNCAL 133
QY 166 PIYKREYREGDVQLISECAVSAQMMAVDYPS-TLVSRNGAGLTIFSTALSGQYL 224
DB 134 PIVMEYTCYSYKKSIGACPIRTQPRW--NYDSFSAVSEDLGFLMHAPEETAGTYLR 191
QY 225 TLKIGRFQALVTL--VNDRCIKIGSQLNLPSCWTTEDYQTG-----FOG 271
DB 192 LVKINDMTETITQFLIHRKAGSC-KYALPLRIPPSACLSPOAYQGVVDSIGMLPRFIT 250
QY 272 EHLYPADINTRHADVYNGYEDILQRMNNLLRKNPSAPDRPDSVQOEIPAVTKKAG 331
DB 251 ENQRTVAVYSLKLAG-----WH-----GPKAP-YTSTLLPEL-----S 283
QY 332 RPPDAESSEKKAPEDESD-MQAEASGENPALPEDEDETHDPSNDPYYNDMP 390
DB 284 ETPNA--TQPELAPDEPDESALLEDPVGVAPQIPPMHIFSIQDAAPFHPAPPPNMG 341
QY 391 AVIPEETTKSSNAVSMPIFAFVACAVALVGLTW 426
DB 342 LI-----AGAVGGSILALALVIC-----GIYVW 363

RESULT 8
OQ91M3 PRELIMINARY; PRT; 394 AA.
AC OQ91M3;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DE Glycoprotein D.
OS human herpesvirus 1.
CX Alphaherpesvirinae; Simplexvirus.
RN NCBI_TaxID=10298;
RP SEQUENCE FROM N.A.
RA Xiaojuan L., Mingzhao Z.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF33383; AAK19597.1; -.
DR InterPro; IPR002896; Herpes-glycop_D.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF01537; Herpes-glycop_D; 1.
DR PROSITE; PS00266; SOMATOTROPIN_1; UNKNOWN_1.
SQ SEQUENCE 394 AA; 43277 MW; E7294FC19486AC0 CRC64;

Query Match 8.1%; Score 186.5; DB 12; Length 394;
Best Local Similarity 23.2%; Pred. No. 2.5e-07;
Matches 76; Conservative 46; Mismatches 145; Indels 61; Gaps 13;

DY 106 PYNRYLTVSRGCDVVELNPISNVDNMISAKEKEGPFESVWFYIKGDDGEDKYC 165
DB 79 PIVVYAVLERACRSVLNAPSEAPQIVRGASEDVAKOPYNLTIAFRM-----GNCAL 133

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QY 166 PIYKREYRECGDVLSECAVQSAQMAVAVYPS--TLVSRNGAGLTIFSPALSGOYL 224
  || || || || || || || || || || || || || || || || || || || || ||
DB 134 PITVMEYTESYKSLGACPIRTQPRW--NYDSEFSVSEEDLGLMHPAFETAGTYLR 191
QY 225 TLKIGRFAOTALVLE--VNDRCIKIGSQLNLFPSKCWTEQYQYG-----FOG 271
  || || || || || || || || || || || || || || || || || || || || ||
DB 192 LVKINDWEITQFILEHRAKGCSC-KYALPLRLIPRSACLSPOAYQOGVTVDSIGMLPRFIP 250
QY 272 EHLVPIADTNTNRHADVDYRGYEDIIQRNNNLIRKKNPSPDRPDSVPOEIPAVTKKAE 331
  || || || || || || || || || || || || || || || || || || || || ||
DB 251 ENQRTVAVYSLKIAG-----WH-----GPKAP-YTSTLLPEL-----S 283
QY 332 RPPDAESSEKKAPRDESD--MQAEASGENPALPEDEVEDTEHDDPNSDPDYNDMP 390
  || || || || || || || || || || || || || || || || || || || || ||
DB 284 ETPNA--TQPELAPEDPDSALLEDPVGTVAPOIRPNMHIPSIQDAATPYHPAPRPNMG 341
QY 391 AVIPEETTKSSNAVSMPIFAAFVACAV 418
DB 342 LI-----AGAVGSLALVALYICG 360

RESULT 9
QY 091NH6 PRELIMINARY: PRT: 394 AA.
AC 091NH6:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Glycoprotein D.
GN GD.
OS human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN SEQUENCE FROM N.A.
RC STRAIN=F;
RA Lee H.H.;
RT "Cloning, sequencing and baculovirus-based expression of the
RT glycoprotein D gene of Herpes simplex virus type 1 strain F.";
RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF293614; AAK93950.1;
DR InterPro: IPR002896; Herpes_glycop_D.
DR InterPro: IPR001400; Simplexvirus.
DR Pfam: PF05537; Herpes_glycop_D.1.
DR PROSITE: PS00266; SOMATOTROPIN_1; UNKNOWN_1.
SQ SEQUENCE 394 AA; 43344 MW; 541E6C1F9A6EC8 CRC64;

Query Match 8.0%; Score 184; DB 12; Length 394;
Best Local Similarity 24.1%; Pred. No. 4e-07;
Matches 82; Conservative 43; Mismatches 141; Indels 74; Gaps 16;
QY 106 PYNRLTVRSRCGVDELNPISNVDDMTSAKKEKGGPFEASVYVYIKGDGEDKYC 165
  || || || || || || || || || || || || || || || || || || || || ||
DB 79 PITVYAVLERACRSVLNLNAPSEAPQIVRGASEDVKQPYNLTIAMFRN-----GCNCAI 133
QY 166 PIYKREYRECGDVLSECAVQSAQMAVAVYPS--TLVSRNGAGLTIFSPALSGOYL 224
  || || || || || || || || || || || || || || || || || || || || ||
DB 134 PITVMEYTESYKSLGACPIRTQPRW--NYDSEFSVSEEDLGLMHPAFETAGTYLR 191
QY 225 TLKIGRFAOTALVLE--VNDRCIKIGSQLNLFPSKCWTEQYQYG-----FOG 271
  || || || || || || || || || || || || || || || || || || || || ||
DB 192 LVKINDWEITQFILEHRAKGCSC-KYALPLRLIPRSACLSPOAYQOGVTVDSIGMLPRFIP 250
QY 272 EHLVPIADTNTNRHADVDYRGYEDIIQRNNNLIRKKNPSPDRPDSVPOEIPAVTKKAE 331
  || || || || || || || || || || || || || || || || || || || || ||
DB 251 ENQRTVAVYSLKIAG-----WH-----GPKAP-YTSTLLPEL-----S 283
QY 332 RPPDAESSEKKAPRDESD--MQAEASGENPALPEDEVEDTEHDDPNSDPDYNDMP 390
  || || || || || || || || || || || || || || || || || || || || ||
DB 284 ETPNA--TQPELAPEDPDSALLEDPV-----GTVAPOIRPNMHIPSIQDAATPYHPAPR 337
QY 387 NDMPAVIPEETTKSSNAVSMPIFAAFVACAVALVGLIYW 426

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DB 338 NMHGLI-----AGAVGSLALVALYIC-----GIYVW 363

RESULT 10
QY 080RB7 PRELIMINARY: PRT: 394 AA.
AC 080RB7:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Glycoprotein D.
GN Glycoprotein D.
OS human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN SEQUENCE FROM N.A.
RC STRAIN=KHS1;
RA Kim J.K., Kim Y.K., Hong J.B., Kim S.Y., Ahn J.K.;
RT "Isolation of the enhanced neurovirulent HSV-1 strains from Korean
RT patients.";
RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF487901; AAL90883.1;
SQ SEQUENCE 394 AA; 43240 MW; 725F6AC2B66848FC CRC64;

Query Match 7.8%; Score 180; DB 12; Length 394;
Best Local Similarity 22.9%; Pred. No. 8.6e-07;
Matches 77; Conservative 47; Mismatches 146; Indels 66; Gaps 14;
QY 106 PYNRLTVRSRCGVDELNPISNVDDMTSAKKEKGGPFEASVYVYIKGDGEDKYC 165
  || || || || || || || || || || || || || || || || || || || || ||
DB 79 PITVYAVLERACRSVLNLNAPSEAPQIVRGASEDVKQPYNLTIAMFRN-----GCNCAI 133
QY 166 PIYKREYRECGDVLSECAVQSAQMAVAVYPS--TLVSRNGAGLTIFSPALSGOYL 224
  || || || || || || || || || || || || || || || || || || || || ||
DB 134 PITVMEYTESYKSLGACPIRTQPRW--NYDSEFSVSEEDLGLMHPAFETAGTYLR 191
QY 225 TLKIGRFAOTALVLE--VNDRCIKIGSQLNLFPSKCWTEQYQYG-----FOG 271
  || || || || || || || || || || || || || || || || || || || || ||
DB 192 LVKINDWEITQFILEHRAKGCSC-KYALPLRLIPRSACLSPOAYQOGVTVDSIGMLPRFIP 250
QY 272 EHLVPIADTNTNRHADVDYRGYEDIIQRNNNLIRKKNPSPDRPDSVPOEIPAVTKKAE 331
  || || || || || || || || || || || || || || || || || || || || ||
DB 251 ENQRTVAVYSLKIAG-----WH-----GPKAP-YTSTLLPEL-----S 283
QY 332 RPPDAESSEKKAPRDESD--MQAEASGENPALPEDEVEDTEHDDPNSDPDYNDMP 390
  || || || || || || || || || || || || || || || || || || || || ||
DB 284 ETPNA--TQPELAPEDPDSALLEDPVGTVAPOIRPNMHIPSIQDAATPYHPAPRPNMG 341
QY 391 AVIPEETTKSSNAVSMPIFAAFVACAVALVGLIYW 426
DB 342 LI-----AGAVGSLALVALYIC-----GIYVW 363

RESULT 11
QY 004245 PRELIMINARY: PRT: 402 AA.
AC 004245:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Glycoprotein D precursor.
OS Equine herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10326;
RN SEQUENCE FROM N.A.
RC MEDLINE=92180315; Pubmed=1665613;
RA Whalley J.M., Robertson G., Bell C.W., Love D., Elphinstone M.,
RA Wiley L., Craven D.;
RT "Identification and comparative sequence analysis of a gene in equine

```

herpesvirus 1 with homology to the herpes simplex virus glycoprotein D gene.";
 RL Virus Genes 5:313-325(1991).
 DR EMBL; M59773; AAA46080.1; "-
 DR InterPro; IPR002896; Herpes_glycop_D.
 DR Pfam; PF01537; Herpes_glycop_D; 1.
 KM Signal; glycoprotein.
 FT SIGNAL 1 26
 FT CHAIN 27 402
 FT CAROHD 53 402
 FT CAROHD 61 61
 FT CAROHD 297 297
 FT CAROHD 346 346
 FT CAROHD 402 AA; 45239 MW; 546F97A05E1B1E0 CRC64;
 SQ SEQUENCE

Query Match 7.6%; Score 175; DB 12; Length 402;
 Best Local Similarity 22.6%; Pred. No. 2,3e-06;
 Matches 84; Conservative 53; Mismatches 149; Indels 86; Gaps 17;

QY 87 YDY-ILGRALDALTPAVGP-----YNNRYLFRVSRGCDVVELNPISNVDMISAKEK 141
 Db 52 YNTTLITRYNATVALASPFINOVKNWDLRIYATRPCEMIALIAKTINDSLKELAAAK 111
 QY 142 GPFPEASVYMFYVIGDGDGDKYC--PIYRKREKCGVOLLSECAVQSAQMNAVDPVS 199
 Db 112 --TYARLTWTKIM-----PTCATPIHDVSYMCNPKLSFAMCDESDILMOASLITM 162
 QY 200 TLVSRNGAGLTIFSPPTAALSGOYLTLTKI--GRFAQTALVTEVNDRCIKISQINF--LPS 257
 Db 163 AAEITDELGLVLAAPAHASAGLYRVEIIDRRITDTSVITPBERC-PIAFEONFGNPD 221
 QY 258 KCMTEQOQNG-----FQGEHLPIADTNRHADVDYRGYEDILQRM-----NNLNRK- 305
 Db 222 KCKTPEOYSRGEVTRRLRFLGEFNPPQGEHMT-----WLKFMFYDGNLPLQF 269
 QY 306 -----KNPSADPRP--DSVPOEIPAVTKAEGRTPDASESEKAPPESEDDMQAEAS 357
 Db 270 YEQAFAFPVPPDNNPGDSVSEI-----TQKTDPKPQADPKPNQP 313
 QY 358 GENA---ALPEDEVPEDTEHDDPNSDPDYNDMPAVIPEETTKSSNAVMPITFAFV 414
 Db 314 EKMPISIKHLAPRLDEVEDEVIE-----PYTKPKPK--TSKSNSTFGVISTVGLG 357
 QY 415 ACAVALYGLVW 426
 Db 358 IAGLVIVGLV 369

RESULT 12
 Q91W02 PRELIMINARY; PRT; 400 AA.

AC Q91W02
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
 DE glycoprotein D.
 GN GD.
 OS Pseudorabies virus (strain Kaplan) (PRV).
 OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicelloviruses.
 OX NCB1_TaxID=33703;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KAPLAN.
 RX MEDLINE-20219392; PubMed-10756012;
 RA Brack A.R., Klupp B.G., Granzow H., Ttirabassi R., Engquist L.W.,
 Mettenleiter T.C.;
 RT "Role of the cytoplasmic tail of pseudorabies virus glycoprotein e in
 RT virion formation.";
 RL J. Virol. 74:4004-4016(2000).
 DR EMBL; AJ271966; CAB72453.1; "-
 DR InterPro; IPR002896; Herpes_glycop_D.
 DR Pfam; PF01537; Herpes_glycop_D; 1.
 DR PRINTS; PRO1217; PRICHEXTNSN.
 DR InterPro; IPR002965; P_rich_extensn.

DR Pfam; PF01537; Herpes_glycop_D; 1.
 DR PRINTS; PRO1217; PRICHEXTNSN.
 SQ SEQUENCE 400 AA; 44338 MW; E5D3BF94976F1C7E CRC64;
 Query Match 7.3%; Score 169; DB 12; Length 400;
 Best Local Similarity 21.2%; Pred. No. 7,3e-06;
 Matches 90; Conservative 54; Mismatches 152; Indels 128; Gaps 20;

QY 73 LLSFASQSTAAVYDYTLG-----RRALDALTPAVGPYRRLYLR--VSRG 117
 Db 6 LLAAVATTTGADVADVAPAPFPAPPVPTYESMQTLITVPSFVGADVYHTRLPEDP 65
 QY 118 CDVVELNPISNVDMISAKEKCGPFPEASVYMFYIKDGDGDKYC--IYRKREK 175
 Db 66 CGVALISDPQVDRLLDEAAVHRR--PTYRAHVAVYRIADG-----CAHLVFIIEYADC 117
 QY 176 GDVOLLSECAVQSAQM---AVDVPSLTVSRNGAGLTIFSPPTAALSGOY--LTLTKIGR 230
 Db 118 DPROIFGRCRRRTPTPMWTPSADYMFPT---EDELGLMTAPGRFNEGQYRLVSYDGVN 174
 QY 231 FAQTALVTEVNDRC--LKTGSQINFPSKWTTEOYQTFQGEHLPIADTNRHADY 288
 Db 175 ILTDFVVALPEGQECPPARVDQRTYKFGACMWDSEFRGCV-----DY 217
 QY 289 YR-----GYEDILQRMNNLLRKN-----PSA-----PDPRP 315
 Db 218 MRFITPPEYQPPHREVVNYM-----YRNGRTLPRAVAAATPAIDPARPSAGSPRRPRP 273
 QY 316 DSVPOEIPA--VTKAEGRTPDASESEKAPPESEDDMQAEASGENAPALPEDEVEDET 374
 Db 274 RPRPKPEPAVTPAPPCGRLEPATRD-----HAAGHPTRPRPRPEFPH-- 317
 QY 375 EHDPPNSDPDYNDMPAVI-----PYEETTKSSNAYS---MDIFAPACAVALVG 422
 Db 318 ---RPRAP-----PAVPSGMPDPAEPFOPRTPAAPGSRHSRYIVGTGAMGALLVG 367
 QY 423 LLYW 426
 Db 368 VCXY 371

RESULT 13
 Q91W00 PRELIMINARY; PRT; 516 AA.

AC Q91W00
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
 DE Hybrid protein.
 GN MURANT GDIE.
 OS Pseudorabies virus (strain Kaplan) (PRV).
 OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicelloviruses.
 OX NCB1_TaxID=33703;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KAPLAN.
 RX MEDLINE-20219392; PubMed-10756012;
 RA Brack A.R., Klupp B.G., Granzow H., Ttirabassi R., Engquist L.W.,
 Mettenleiter T.C.;
 RT "Role of the cytoplasmic tail of pseudorabies virus glycoprotein e in
 RT virion formation.";
 RL J. Virol. 74:4004-4016(2000).
 DR EMBL; AJ271967; CAB72452.1; "-
 DR InterPro; IPR003404; Herpes_glycopE.
 DR InterPro; IPR002896; Herpes_glycopE.
 DR InterPro; IPR002965; P_rich_extensn.
 DR Pfam; PF02480; Herpes_gE; 1.
 DR Pfam; PF01537; Herpes_glycop_D; 1.
 DR PRINTS; PRO1217; PRICHEXTNSN.
 DR SEQUENCE 516 AA; 56874 MW; 87312C43E7EF7ED CRC64;
 Query Match 7.3%; Score 169; DB 12; Length 516;

RESULT 14			
ID	089634	PRELIMINARY;	PRT; 374 AA.
AC	089634;		
DT	01-NOV-1996 (TrEMBLrel. 01, Created)		
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)		
DE	Glycoprotein GD.		
OS	Feline herpesvirus (Feld herpesvirus 1).		
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;		
OX	Alphaherpesvirinae; Varicellovirus.		
OX	NCBI_TaxID=10334;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=94267406; PubMed=8207390;		
RA	Spatz S.J., Rota P.A., Maes R.K.;		
RT	"Identification of the feline herpesvirus type 1 (FHV-1) genes		
RT	encoding glycoproteins G, D, I and E: expression of FHV-1 glycoprotein		
RT	in vacuola and raccoon poxviruses.";		
RL	J. Gen. Virol. 75:1235-1244(1994).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C7301;		
RX	MEDLINE=94303154; PubMed=8030205;		
RA	Medea K., Kawaguchi Y., Ono M., Inoshima Y., Miyazawa T., Tanya Y.,		
RT	Kai C., Mikami T.;		
RT	"A gp homologous gene of feline herpesvirus type 1 encodes a		
RT	hemagglutinin (gp60).";		
RL	Virology 202:1034-1038(1994).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=G2620;		
RA	Sondermeijer P.J.A.;		
RT	Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.		
RP	[4]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=G2620;		

	RESULT 15		
09YS31			
ID	09YS31	PRELIMINARY;	PRT: 398 AA.
AC	09YS31		
DT	01-MAY-1999 (TEMBLrel. 10, Created)		
DT	01-MAY-1999 (TEMBLrel. 10, Last sequence update)		
DT	01-JUN-2001 (TEMBLrel. 17, Last annotation update)		
DE	Glycoprotein gp50.		
OS	Pseudocrabes virus.		
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;		
OC	Alphaherpesvirinae; Varicellovirus.		
OX	NCBI_TaxID=10345;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=HUBel;		
RA	Wang J.F., Zhang C.-Y., Ding J.H., Zhou R., Wen S.Z., Huang Z.H.		
RT	"Cloning and sequence analysis of glycoprotein gp50 gene of		
RT	pseudocrabes virus strain HUBel."		
RL	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF092447; AAC6904.1;		
DR	InterPro: IPR002896; Herpes_glycop.D.		
DR	InterPro: IPR002965; P_tichl.exctenn.		
Pfam:	PF01537; Herpes_glycop_D_1.		

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OM protein - protein search, using sw model

Run on: February 19, 2003, 16:21:11 ; Search time 18 seconds
(without alignments)
709,419 Million cell updates/sec

Title: US-09-994-064-11

Sequence: 1 MHRPHRRSRYYAKGEVLN.....ACAVLVGLWISYWCARS 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgnt2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgnt2_6/prodata/1/1aa/5B_COMB.pep:*
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6: /cgnt2_6/prodata/1/1aa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2311	100.0	434	2	US-08-484-575A-20
2	2311	100.0	434	3	US-08-477-459-20
3	2311	100.0	434	3	US-08-479-869-20
4	2311	100.0	434	4	US-08-486-414-46
5	2311	100.0	434	4	PCT-US94-01826A-20
6	2311	100.0	434	5	PCT-US94-02252A-20
7	2311	100.0	434	5	PCT-US96-03916-11
8	2311	100.0	434	5	PCT-US96-03916-67
9	772	33.4	144	4	US-08-486-414-20
10	196	8.5	393	1	US-08-220-151-23
11	196	8.5	393	1	US-08-413-118-23
12	196	8.5	393	3	US-08-473-446-23
13	190	8.2	369	2	US-08-139-609-1
14	190	8.2	394	1	US-08-499-568-4
15	190	8.2	394	2	US-08-793-958-4
16	184.5	8.0	442	6	5470718-2
17	183.5	7.9	393	6	5182195-10
18	181.5	7.9	383	6	5470718-5
19	181	7.8	442	1	US-08-220-151-22
20	181	7.8	442	1	US-08-413-118-22
21	181	7.8	442	3	US-08-473-446-22
22	181	7.8	442	6	5470718-3
23	179	7.7	388	1	US-08-499-568-11
24	179	7.7	388	2	US-08-793-958-11
25	165.5	7.2	308	2	US-08-499-568-2
26	165.5	7.2	308	2	US-08-793-958-2
27	165	7.1	402	6	5352575-5

28	162.5	7.0	373	3	US-08-911-321-9	Sequence 9, App1
29	162.5	7.0	373	5	PCT-US95-13975-73	Sequence 73, App1
30	162.5	7.0	374	1	US-08-220-151-21	Sequence 21, App1
31	162.5	7.0	374	1	US-08-413-118-21	Sequence 21, App1
32	162.5	7.0	374	3	US-08-473-446-21	Sequence 21, App1
33	159	6.9	393	1	US-08-499-568-15	Sequence 15, App1
34	159	6.9	393	2	US-08-793-958-15	Sequence 15, App1
35	158	6.8	393	2	US-08-956-998-2	Sequence 2, App1
36	157	6.8	368	5	PCT-US93-11703-24	Sequence 24, App1
37	147	6.4	366	6	5470718-4	Sequence 6, App1
38	144	6.2	417	2	US-08-682-847-6	Sequence 2, App1
39	144	6.2	417	4	US-09-063-676-2	Sequence 2, App1
40	125	5.4	345	1	US-08-220-151-19	Sequence 19, App1
41	125	5.4	345	1	US-08-220-151-20	Sequence 20, App1
42	125	5.4	345	1	US-08-413-118-19	Sequence 19, App1
43	125	5.4	345	1	US-08-413-118-20	Sequence 20, App1
44	125	5.4	345	1	US-08-413-118-128	Sequence 128, App
45	125	5.4	345	1	US-08-680-726A-54	Sequence 54, App

ALIGNMENTS

RESULT 1
US-08-484-575A-20
; Sequence 20, Application US/08484575A
; Patent No. 5925358
; GENERAL INFORMATION:
; APPLICANT: Mark D. Cochran and David E. Junker
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,575A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0450
; TELEFAX: (212)391-0525
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-575A-20
Query Match 100.0%; Score 2311; DB 2; Length 434;
Best Local Similarity 100.0%; Pred No. 4e-233;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MHRPHRRSRYYAKGEVLNKKHNDCCGKRCSCAAVFTLFWTCVRIMREHICFVRNAMDR 60
Db 1 MHRPHRRSRYYAKGEVLNKKHNDCCGKRCSCAAVFTLFWTCVRIMREHICFVRNAMDR 60
OY 61 HLFRLNFWTIVLLISFASOSTAAVYDYTLGRRALDALTIPAVGPNRYLTVNSGCDV 120
Db 61 HLFRLNFWTIVLLISFASOSTAAVYDYTLGRRALDALTIPAVGPNRYLTVNSGCDV 120
OY 121 VELNPLISNVDDMTSAKEREKGGPFEEASVYVFWVINGDGDGDKYCPYIRKREYRGGCDVYL 180

121 VELNPISNVDDMTSAAKEKEKGGPFEEASVWYFVIKGDGEDKCYPIYRKREYRECGDVOL 180
181 LSECAVQSAQMAWADVVPSTLVSRNAGLTFSPALSGOYLTLTKIGRFAQTALVTL 240
181 LSECAVQSAQMAWADVVPSTLVSRNAGLTFSPALSGOYLTLTKIGRFAQTALVTL 240
241 VNRCLKIGSQLNLFPSKCMWTEQYQTFGEHLYPIADTNRHADVYRGYEDILORRN 300
241 VNRCLKIGSQLNLFPSKCMWTEQYQTFGEHLYPIADTNRHADVYRGYEDILORRN 300
301 NLRRKNPSAPDRPSPVQEIPIAVTKKAGRTPDASESEKKAPEPDESDMOAASGEN 360
301 NLRRKNPSAPDRPSPVQEIPIAVTKKAGRTPDASESEKKAPEPDESDMOAASGEN 360
361 PALPDEDEVPEDTEHDDNSDPDYNDMPAVIPEETTKSSNAVSMPIFAAFVACAVAL 420
361 PALPDEDEVPEDTEHDDNSDPDYNDMPAVIPEETTKSSNAVSMPIFAAFVACAVAL 420
421 VGLLWMSIVKARS 434
421 VGLLWMSIVKARS 434

RESULT 2

US-08-477-459-20
Sequence 20, Application US/08477459
Patent No. 6001369
GENERAL INFORMATION:
APPLICANT: Mark D. Cochran
TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses
TITLE OF INVENTION: Thee of
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,459
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-459-20

Query Match 100.0%; Score 2311; DB 3; Length 434;
Best Local Similarity 100.0%; Pred. No. 4e-233;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MHRPRLRHSRYAKGEVLNKHMDGGRCCGSAVFTLFTCVIRREHICFVRNAMD 60
1 MHRPRLRHSRYAKGEVLNKHMDGGRCCGSAVFTLFTCVIRREHICFVRNAMD 60
61 HLFENAFWTIVLSSFSQSTAAVTYDILGRALDALTIPAVCPYRKYLRVSGDV 120
61 HLFENAFWTIVLSSFSQSTAAVTYDILGRALDALTIPAVCPYRKYLRVSGDV 120

121 VELNPISNVDDMTSAAKEKEKGGPFEEASVWYFVIKGDGEDKCYPIYRKREYRECGDVOL 180
121 VELNPISNVDDMTSAAKEKEKGGPFEEASVWYFVIKGDGEDKCYPIYRKREYRECGDVOL 180
181 LSECAVQSAQMAWADVVPSTLVSRNAGLTFSPALSGOYLTLTKIGRFAQTALVTL 240
181 LSECAVQSAQMAWADVVPSTLVSRNAGLTFSPALSGOYLTLTKIGRFAQTALVTL 240
241 VNRCLKIGSQLNLFPSKCMWTEQYQTFGEHLYPIADTNRHADVYRGYEDILORRN 300
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301 NLRRKNPSAPDRPSPVQEIPIAVTKKAGRTPDASESEKKAPEPDESDMOAASGEN 360
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361 PALPDEDEVPEDTEHDDNSDPDYNDMPAVIPEETTKSSNAVSMPIFAAFVACAVAL 420
361 PALPDEDEVPEDTEHDDNSDPDYNDMPAVIPEETTKSSNAVSMPIFAAFVACAVAL 420
421 VGLLWMSIVKARS 434
421 VGLLWMSIVKARS 434

RESULT 3

US-08-479-869-20
Sequence 20, Application US/08479869
Patent No. 6123949
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D, Mark D
TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,869
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/024,156
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-869-20

Query Match 100.0%; Score 2311; DB 3; Length 434;
Best Local Similarity 100.0%; Pred. No. 4e-233;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MHRPRLRHSRYAKGEVLNKHMDGGRCCGSAVFTLFTCVIRREHICFVRNAMD 60

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|||||
Db 1 MHRPRLRRHSRYAKGEVLNKHMDCCGKRCSCGAATFTLFTVCVIRIMEHICFVRNAMD 60
QY 61 HLFIRNAFWTIVLLSSFAASOSTAAVTYDYLIGRRALDALITPAVGPNRYLTRVSRGCDV 120
Db 61 HLFIRNAFWTIVLLSSFAASOSTAAVTYDYLIGRRALDALITPAVGPNRYLTRVSRGCDV 120
QY 121 VELNPISNVDDMISAKEKEKGPEASVWFYIKGDGDEKXCPIYRKEYRECGDVOL 180
Db 121 VELNPISNVDDMISAKEKEKGPEASVWFYIKGDGDEKXCPIYRKEYRECGDVOL 180
QY 181 LSECAYOAOQWMAVDYVSTLVSRNAGLITFSPALSGOYLTLTKIGRPAQTALVTL 240
Db 181 LSECAYOAOQWMAVDYVSTLVSRNAGLITFSPALSGOYLTLTKIGRPAQTALVTL 240
QY 241 VNRCLKIGSQLNPLPSKCWTTTEOYQTGFOGEHLYPADNTNRHADVYRGYEDILQRMN 300
Db 241 VNRCLKIGSQLNPLPSKCWTTTEOYQTGFOGEHLYPADNTNRHADVYRGYEDILQRMN 300
QY 301 NLKRKNPSADPPRDSVPOETPAVTKAEGRTDPAESSEKKAPPESEDDMOAEASGEN 360
Db 301 NLKRKNPSADPPRDSVPOETPAVTKAEGRTDPAESSEKKAPPESEDDMOAEASGEN 360
QY 361 PALPEDEVEDETHDDPNSDPDYNDMPAVIPVEETTKSSNAVSMPIFAAFVACAVAL 420
Db 361 PALPEDEVEDETHDDPNSDPDYNDMPAVIPVEETTKSSNAVSMPIFAAFVACAVAL 420
QY 421 VGLLWSTIVKCAR 434
Db 421 VGLLWSTIVKCAR 434
```

```
RESULT 4
US-08-486-414-46
: Sequence 46, Application US/08486414B
: Patent No. 6136318
: GENERAL INFORMATION:
: APPLICANT: Cochran, Mark D.
: TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES AND USES THEREOF
: FILE REFERENCE: 42771D
: CURRENT APPLICATION NUMBER: US/08/486, 414B
: CURRENT FILING DATE: 1995-06-07
: NUMBER OF SEQ ID NOS: 46
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 46
: LENGTH: 434
: TYPE: PRT
: ORGANISM: Fowlpox virus
US-08-486-414-46
```

```
Query Match 100.0%; Score 2311; DB 4; Length 434;
Best Local Similarity 100.0%; Pred. No. 4e-233;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRPRLRRHSRYAKGEVLNKHMDCCGKRCSCGAATFTLFTVCVIRIMEHICFVRNAMD 60
Db 1 MHRPRLRRHSRYAKGEVLNKHMDCCGKRCSCGAATFTLFTVCVIRIMEHICFVRNAMD 60
QY 61 HLFIRNAFWTIVLLSSFAASOSTAAVTYDYLIGRRALDALITPAVGPNRYLTRVSRGCDV 120
Db 61 HLFIRNAFWTIVLLSSFAASOSTAAVTYDYLIGRRALDALITPAVGPNRYLTRVSRGCDV 120
QY 121 VELNPISNVDDMISAKEKEKGPEASVWFYIKGDGDEKXCPIYRKEYRECGDVOL 180
Db 121 VELNPISNVDDMISAKEKEKGPEASVWFYIKGDGDEKXCPIYRKEYRECGDVOL 180
QY 181 LSECAYOAOQWMAVDYVSTLVSRNAGLITFSPALSGOYLTLTKIGRPAQTALVTL 240
Db 181 LSECAYOAOQWMAVDYVSTLVSRNAGLITFSPALSGOYLTLTKIGRPAQTALVTL 240
QY 241 VNRCLKIGSQLNPLPSKCWTTTEOYQTGFOGEHLYPADNTNRHADVYRGYEDILQRMN 300
Db 241 VNRCLKIGSQLNPLPSKCWTTTEOYQTGFOGEHLYPADNTNRHADVYRGYEDILQRMN 300
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Db 241 VNRCLKIGSQLNPLPSKCWTTTEOYQTGFOGEHLYPADNTNRHADVYRGYEDILQRMN 300
QY 301 NLKRKNPSADPPRDSVPOETPAVTKAEGRTDPAESSEKKAPPESEDDMOAEASGEN 360
Db 301 NLKRKNPSADPPRDSVPOETPAVTKAEGRTDPAESSEKKAPPESEDDMOAEASGEN 360
QY 361 PALPEDEVEDETHDDPNSDPDYNDMPAVIPVEETTKSSNAVSMPIFAAFVACAVAL 420
Db 361 PALPEDEVEDETHDDPNSDPDYNDMPAVIPVEETTKSSNAVSMPIFAAFVACAVAL 420
QY 421 VGLLWSTIVKCAR 434
Db 421 VGLLWSTIVKCAR 434
```

```
RESULT 5
PCT-US94-01826A-20
: Sequence 20, Application PC/TUS9401826A
: GENERAL INFORMATION:
: APPLICANT: Syntro Corporation, et al.
: TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPv-043 and Uses Thereof
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: John P. White
: STREET: 30 Rockefeller Plaza
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10112
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/01826A
: FILING DATE: 28-FEB-1994
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: White Esq, John P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212)977-9550
: TELEFAX: (212)664-0525
: TELEX: 422523
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 434 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
PCT-US94-01826A-20
```

```
Query Match 100.0%; Score 2311; DB 5; Length 434;
Best Local Similarity 100.0%; Pred. No. 4e-233;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRPRLRRHSRYAKGEVLNKHMDCCGKRCSCGAATFTLFTVCVIRIMEHICFVRNAMD 60
Db 1 MHRPRLRRHSRYAKGEVLNKHMDCCGKRCSCGAATFTLFTVCVIRIMEHICFVRNAMD 60
QY 61 HLFIRNAFWTIVLLSSFAASOSTAAVTYDYLIGRRALDALITPAVGPNRYLTRVSRGCDV 120
Db 61 HLFIRNAFWTIVLLSSFAASOSTAAVTYDYLIGRRALDALITPAVGPNRYLTRVSRGCDV 120
QY 121 VELNPISNVDDMISAKEKEKGPEASVWFYIKGDGDEKXCPIYRKEYRECGDVOL 180
Db 121 VELNPISNVDDMISAKEKEKGPEASVWFYIKGDGDEKXCPIYRKEYRECGDVOL 180
QY 181 LSECAYOAOQWMAVDYVSTLVSRNAGLITFSPALSGOYLTLTKIGRPAQTALVTL 240
Db 181 LSECAYOAOQWMAVDYVSTLVSRNAGLITFSPALSGOYLTLTKIGRPAQTALVTL 240
QY 241 VNRCLKIGSQLNPLPSKCWTTTEOYQTGFOGEHLYPADNTNRHADVYRGYEDILQRMN 300
Db 241 VNRCLKIGSQLNPLPSKCWTTTEOYQTGFOGEHLYPADNTNRHADVYRGYEDILQRMN 300
```

Db 241 VNRCLKIGSOLNLPSCKMTTEQYOTGFOGEHLIPIADTNTRHADVYRGYEDILQRMN 300
QY 301 NLRRKNPSADPPRDSVPOEIPAVTKKAGRTPPAESSEKKAPPESEDDMOAASGEN 360
Db 301 NLRRKNPSADPPRDSVPOEIPAVTKKAGRTPPAESSEKKAPPESEDDMOAASGEN 360
QY 361 PALPEDEVEDEHDDPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAFVACAVALL 420
Db 361 PALPEDEVEDEHDDPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAFVACAVALL 420
QY 421 VGLLWMSIVKCAR 434
Db 421 VGLLWMSIVKCAR 434

RESULT 6
PCT-US94-02252A-20

; Sequence 20, Application PC/TUS9402252A
; GENERAL INFORMATION:
; APPLICANT: Syntro Corporation, et al.
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02252A
; FILING DATE: 28-FEB-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-02252A-20

Query Match 100.0%; Score 2311; DB 5; Length 434;
Best Local Similarity 100.0%; Pred. No. 4e-233;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPHLRHSRYAKGEVLNKHMDCCGKRCGSAVFTLFTVCVIRIMREHICFVNAMDR 60
Db 1 MRPHLRHSRYAKGEVLNKHMDCCGKRCGSAVFTLFTVCVIRIMREHICFVNAMDR 60
QY 61 HFLRNAFTIYLLSSFASSOSTAAVYDYLGRALDALITPAVGPYNRILTRVSRGCDV 120
Db 61 HFLRNAFTIYLLSSFASSOSTAAVYDYLGRALDALITPAVGPYNRILTRVSRGCDV 120
QY 121 VELNPISNVDDMISAKEKKGPEFASVWVFYIKGDDGEDKCYPIYRKREYREGCDV 180
Db 121 VELNPISNVDDMISAKEKKGPEFASVWVFYIKGDDGEDKCYPIYRKREYREGCDV 180
QY 181 LSECVAQSAQMAVDPVSTLVSRNGAGLITFPTAALSGOYLLTLKIGRFAQTALVTLE 240
Db 181 LSECVAQSAQMAVDPVSTLVSRNGAGLITFPTAALSGOYLLTLKIGRFAQTALVTLE 240

QY 241 VNRCLKIGSOLNLPSCKMTTEQYOTGFOGEHLIPIADTNTRHADVYRGYEDILQRMN 300
Db 241 VNRCLKIGSOLNLPSCKMTTEQYOTGFOGEHLIPIADTNTRHADVYRGYEDILQRMN 300
QY 301 NLRRKNPSADPPRDSVPOEIPAVTKKAGRTPPAESSEKKAPPESEDDMOAASGEN 360
Db 301 NLRRKNPSADPPRDSVPOEIPAVTKKAGRTPPAESSEKKAPPESEDDMOAASGEN 360
QY 361 PALPEDEVEDEHDDPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAFVACAVALL 420
Db 361 PALPEDEVEDEHDDPNSDPDYNDMPAVIPEETTKSSNAVSMPIFAFVACAVALL 420
QY 421 VGLLWMSIVKCAR 434
Db 421 VGLLWMSIVKCAR 434

RESULT 7
PCT-US96-03916-11

; Sequence 11, Application PC/TUS9603916
; GENERAL INFORMATION:
; APPLICANT: Wild, Martha A.
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03916
; FILING DATE: 23-MAR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,597
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39116-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-03916-11

Query Match 100.0%; Score 2311; DB 5; Length 434;
Best Local Similarity 100.0%; Pred. No. 4e-233;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPHLRHSRYAKGEVLNKHMDCCGKRCGSAVFTLFTVCVIRIMREHICFVNAMDR 60
Db 1 MRPHLRHSRYAKGEVLNKHMDCCGKRCGSAVFTLFTVCVIRIMREHICFVNAMDR 60
QY 61 HFLRNAFTIYLLSSFASSOSTAAVYDYLGRALDALITPAVGPYNRILTRVSRGCDV 120
Db 61 HFLRNAFTIYLLSSFASSOSTAAVYDYLGRALDALITPAVGPYNRILTRVSRGCDV 120
QY 121 VELNPISNVDDMISAKEKKGPEFASVWVFYIKGDDGEDKCYPIYRKREYREGCDV 180

Db 121 VELNPISNVDMISAKEKEGPFESVWFYIKGDDGDKCPYRKREYRCGCVOL 180
OY 181 LSECAVSAQMMAVDYVSTLVSRNGAGLTIFSPALSGOYLTLTKIGRPAQTALVTL 240
Db 181 LSECAVSAQMMAVDYVSTLVSRNGAGLTIFSPALSGOYLTLTKIGRPAQTALVTL 240
OY 241 VNRCLKIGSOLNLPKSCWTEQYOTGFOGHEHLYPIADNTRHADVYRGYEDIIQRMN 300
Db 241 VNRCLKIGSOLNLPKSCWTEQYOTGFOGHEHLYPIADNTRHADVYRGYEDIIQRMN 300
OY 301 NLKRNKPSAPDPRDPSVPOEIPAVTKKAGRTPDAESSEKAPPESEDMDQAESGEN 360
Db 301 NLKRNKPSAPDPRDPSVPOEIPAVTKKAGRTPDAESSEKAPPESEDMDQAESGEN 360
OY 361 PALPEDEVEPEDTEHDDPNSDPDYNDMPAVIPVEETKSSNAVSMPIFAAFVACAVAL 420
Db 361 PALPEDEVEPEDTEHDDPNSDPDYNDMPAVIPVEETKSSNAVSMPIFAAFVACAVAL 420
OY 421 VGLLWMSIVKCARS 434
Db 421 VGLLWMSIVKCARS 434

RESULT 8
PCT-US96-03916-67

Sequence 67, Application PC/TUS9603916
GENERAL INFORMATION:
APPLICANT: Wild, Martha A.
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03916
FILING DATE: 23-MAR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,597
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39116-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-03916-67

Query Match 100.0%; Score 2311; DB 5; Length 434;
Best Local Similarity 100.0%; Pred. No. 4e-233;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MHRPHLRHRSRYAKGEVLNKHMDCCGRCGSGAAVFTLFWTCVIRIREHICFVRNAMDR 60
|||||

Db 1 MHRPHLRHRSRYAKGEVLNKHMDCCGRCGSGAAVFTLFWTCVIRIREHICFVRNAMDR 60
OY 61 HLFRLNAFWTIVLLSFASSOSTAAVYDYILGRALDALTPAVGPYRNYLTRVSRGCDV 120
Db 61 HLFRLNAFWTIVLLSFASSOSTAAVYDYILGRALDALTPAVGPYRNYLTRVSRGCDV 120
OY 121 VELNPISNVDMISAKEKEGPFESVWFYIKGDDGDKCPYRKREYRCGCVOL 180
Db 121 VELNPISNVDMISAKEKEGPFESVWFYIKGDDGDKCPYRKREYRCGCVOL 180
OY 181 LSECAVSAQMMAVDYVSTLVSRNGAGLTIFSPALSGOYLTLTKIGRPAQTALVTL 240
Db 181 LSECAVSAQMMAVDYVSTLVSRNGAGLTIFSPALSGOYLTLTKIGRPAQTALVTL 240
OY 241 VNRCLKIGSOLNLPKSCWTEQYOTGFOGHEHLYPIADNTRHADVYRGYEDIIQRMN 300
Db 241 VNRCLKIGSOLNLPKSCWTEQYOTGFOGHEHLYPIADNTRHADVYRGYEDIIQRMN 300
OY 301 NLKRNKPSAPDPRDPSVPOEIPAVTKKAGRTPDAESSEKAPPESEDMDQAESGEN 360
Db 301 NLKRNKPSAPDPRDPSVPOEIPAVTKKAGRTPDAESSEKAPPESEDMDQAESGEN 360
OY 361 PALPEDEVEPEDTEHDDPNSDPDYNDMPAVIPVEETKSSNAVSMPIFAAFVACAVAL 420
Db 361 PALPEDEVEPEDTEHDDPNSDPDYNDMPAVIPVEETKSSNAVSMPIFAAFVACAVAL 420
OY 421 VGLLWMSIVKCARS 434
Db 421 VGLLWMSIVKCARS 434

RESULT 9

US-08-486-414-20
Sequence 20, Application US/08486414B
Patent No. 6136318
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES AND USES THEREOF
FILE REFERENCE: 42771D
CURRENT APPLICATION NUMBER: US/08/486,414B
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 144
TYPE: PRT
ORGANISM: Fowlpox virus
US-08-486-414-20

Query Match 33.4%; Score 772; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 6.9e-73;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MHRPHLRHRSRYAKGEVLNKHMDCCGRCGSGAAVFTLFWTCVIRIREHICFVRNAMDR 60
Db 1 MHRPHLRHRSRYAKGEVLNKHMDCCGRCGSGAAVFTLFWTCVIRIREHICFVRNAMDR 60
OY 61 HLFRLNAFWTIVLLSFASSOSTAAVYDYILGRALDALTPAVGPYRNYLTRVSRGCDV 120
Db 61 HLFRLNAFWTIVLLSFASSOSTAAVYDYILGRALDALTPAVGPYRNYLTRVSRGCDV 120
OY 121 VELNPISNVDMISAKEKEGPFESVWFYIKGDDGDKCPYRKREYRCGCVOL 180
Db 121 VELNPISNVDMISAKEKEGPFESVWFYIKGDDGDKCPYRKREYRCGCVOL 180
OY 181 LSECAVSAQMMAVDYVSTLVSRNGAGLTIFSPALSGOYLTLTKIGRPAQTALVTL 240
Db 181 LSECAVSAQMMAVDYVSTLVSRNGAGLTIFSPALSGOYLTLTKIGRPAQTALVTL 240

RESULT 10
US-08-220-151-23
Sequence 23, Application US/08220151
Patent No. 5529780
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo

```

APPLICANT: LIMBACH, Keith J.
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C AND 9D AND USES THEREFOR
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,151
FILING DATE: 30-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommet, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-220-151-23

Query Match
Best Local Similarity 8.5%; Score 196; DB I; Length 393;
Matches 79; Conservative 46; Mismatches 138; Indels 66; Gaps 14;

QY 113 RYRSGDYVELNPNISVNDMISAKKEKGGPEASVVFYIKGDGEDKCPYRKEY 172
DB 85 RYRACRSVLLNAPSEAPQIVRGASEDVRRKQPNLTIAFRM-----GCNCALPTVMEY 139
QY 173 RECGDVQLISECAVQSAQMAVADYVPS-TLVSFNGAGLTIFSPALSGOYLTLTKIGRF 231
DB 140 TCSYKKSIGACPIRTQPRM--NYDSEFSAVSEDNLGFIMHAPAFETAGTYLRVAKINDW 197
QY 232 AQTALVTL--VNDRLKIGSQLNPLPSKCTTEOYQYG-----FOGELYPYA 278
DB 198 TETTOFILEHRAKGC-KYTLPLRIPRSACLSPOAYQOGVTVDSIGMLPRFIPENQRTVA 256
QY 279 DYNTRHADYVYGYEDILQRMNNLLRKKNPSPADPRDSVPQETIAPVTKKAGRTPAES 338
DB 257 VYSLKLAG-----WH-----GPRAP-YTSTLLRPELR-----ETPNA-- 287
QY 339 SEKKAPEDESD--MOAESGENPALPEDEDEVEDTEHDDPNSDPDYNDMPAVIYEE 397
DB 288 TQPELAPEDPESALLEDEPVGTVAQIPRNWHLPSIQDAATPYHPRATPNMGLI----- 342
QY 398 TTKSSNAYSNPIFAAFVACAVALLGLVW 426
DB 343 ----AGAVGSSLALALVLC-----GIYVW 362

RESULT 11
US-08-413-118-23
; Sequence 23, Application US/08413118
; Patent No. 5688920
; GENERAL INFORMATION:
; APPLICANT: PAOLETTI, ENZO

```

```

APPLICANT: LIMBACH, KEITH J.
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE, 25TH FLOOR
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,118
FILING DATE: 29-MAR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,151
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-413-118-23

Query Match
Best Local Similarity 8.5%; Score 196; DB I; Length 393;
Matches 79; Conservative 46; Mismatches 138; Indels 66; Gaps 14;

QY 113 RYRSGDYVELNPNISVNDMISAKKEKGGPEASVVFYIKGDGEDKCPYRKEY 172
DB 85 RYRACRSVLLNAPSEAPQIVRGASEDVRRKQPNLTIAFRM-----GCNCALPTVMEY 139
QY 173 RECGDVQLISECAVQSAQMAVADYVPS-TLVSFNGAGLTIFSPALSGOYLTLTKIGRF 231
DB 140 TCSYKKSIGACPIRTQPRM--NYDSEFSAVSEDNLGFIMHAPAFETAGTYLRVAKINDW 197
QY 232 AQTALVTL--VNDRLKIGSQLNPLPSKCTTEOYQYG-----FOGELYPYA 278
DB 198 TETTOFILEHRAKGC-KYTLPLRIPRSACLSPOAYQOGVTVDSIGMLPRFIPENQRTVA 256
QY 279 DYNTRHADYVYGYEDILQRMNNLLRKKNPSPADPRDSVPQETIAPVTKKAGRTPAES 338
DB 257 VYSLKLAG-----WH-----GPRAP-YTSTLLRPELR-----ETPNA-- 287
QY 339 SEKKAPEDESD--MOAESGENPALPEDEDEVEDTEHDDPNSDPDYNDMPAVIYEE 397
DB 288 TQPELAPEDPESALLEDEPVGTVAQIPRNWHLPSIQDAATPYHPRATPNMGLI----- 342
QY 398 TTKSSNAYSNPIFAAFVACAVALLGLVW 426
DB 343 ----AGAVGSSLALALVLC-----GIYVW 362

RESULT 12
US-08-473-446-23
; Sequence 23, Application US/08473446
; Patent No. 6017542

```

GENERAL INFORMATION:
APPLICANT: PAOLETTI, ENZO
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS gb, gc, AND gd AND USES THEREFOR
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE, 25TH FLOOR
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
ZIP: 10036
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,446
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/413,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ. ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-473-446-23

Query Match 8.5%; Score 196; DB 3; Length 393;
Best Local Similarity 24.0%; Pred. No. 6.7e-12;
Matches 79; Conservative 46; Mismatches 138; Indels 66; Gaps 14;

113 RVRGCDVVELNPNISVNDMISAKEKEKGPFEASVWVFYIKGDGDEKCYPIYKEY 172
113 RVRGCDVVELNPNISVNDMISAKEKEKGPFEASVWVFYIKGDGDEKCYPIYKEY 172
85 RVRGCDVVELNPNISVNDMISAKEKEKGPFEASVWVFYIKGDGDEKCYPIYKEY 139
173 RVRGCDVVELNPNISVNDMISAKEKEKGPFEASVWVFYIKGDGDEKCYPIYKEY 231
173 RVRGCDVVELNPNISVNDMISAKEKEKGPFEASVWVFYIKGDGDEKCYPIYKEY 231
140 TEGSYNKSILGACPIRTQPRM--NYDSFSAVSEDNLGLMHAFAFTAGTYLRLVKINDW 197
232 AGRALTYLE--VNDRLKIGSQNLFLPSKWTTEQYTG-----FQGEHLVPIA 278
198 TETTFLEHRAKASC-KYLLPLRIPPSACLSQAYQGVTVDSIGMLPFIENORTVA 256
279 DTMTNRHADVYRGYEDILQRMNLLRKKNSAPDRPDSVPOEIPAVTKKAEGTRPAES 338
257 VYSLKTAG-----WH-----GPRAP-YTSTLLPELP-----ETPMA-- 287
339 SEKKAPPEDESD--MQAEASGENPALPEDEVEPDETHDDPNSDPDYNDMPAVIPVEE 397
288 TOELAPDEDESDALLLEDPAVGAPOIPRMWHTPSIODATPYHPRATNNMGLI----- 342
398 TTKSNASVMPITAFAPACAVALLGLLW 426
343 ---AGAVGSLAALVTC-----GIYVW 362

RESULT 13
US-08-139-609-1

Sequence 1, Application US/08139609
Patent No. 5837249
GENERAL INFORMATION:
APPLICANT: Heder-Katz, Ellen
TITLE OF INVENTION: Method for Generating an Immunogenic T
TITLE OF INVENTION: Cell Response Protective Against a Virus
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/139,609
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/868,946
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/685,459
FILING DATE: 12-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/047,443
FILING DATE: 08-MAY-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/725,087
FILING DATE: 19-APR-1985
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WSTIDUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-139-609-1

Query Match 8.2%; Score 190; DB 2; Length 369;
Best Local Similarity 23.2%; Pred. No. 2.6e-11;
Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;

106 PYNRYLTVRSRCDVVELNPNISVNDMISAKEKEKGPFEASVWVFYIKGDGDEKCY 165
54 PITYVYAVLERACRSVYLLNPAEPQIVRGASEVVRKQPNLTIAFRM-----GGCALI 108
166 PIRKEYREGDQVQLSECAVQSAQMAVAVDVP--TLVSRNGAGLTTFSTALSGOYL 224
109 PITYVYAVLERACRSVYLLNPAEPQIVRGASEVVRKQPNLTIAFRM-----GGCALI 108
225 TLKIGRAQALTYLE--VNDRLKIGSQNLFLPSKWTTEQYTG-----FQGEHLVPIA 271
167 LVKINDWETLTPFLERAKASC-KYALPLRIPPSACLSQAYQGVTVDSIGMLRFRIP 225
272 EHLVPIADNTRHADVYRGYEDILQRMNLLRKKNSAPDRPDSVPOEIPAVTKKAEG 331
226 ENORTVAVYSLKTAG-----WH-----GPRAP-YTSTLLPELP-----S 258
332 RTPDASSEKKAPPEDESD--MQAEASGENPALPEDEVEPDETHDDPNSDPDYNDMP 390

Db 259 ETENA--TOPELAPDEPEDSALLEDPVGTVAPOIPRNMHLSIODATPYHPPATPNNMG 316
QY 391 AVIPEETKSSNAVSMPIFAFVACAVALLVGLLW 426
Db 317 LI-----AGAVGSLIALALVIC-----GIVYW 338

RESULT 14
US-08-499-568-4
Sequence 4, Application US/08499568
Patent No. 5654174
GENERAL INFORMATION:
APPLICANT: Cohen, Gary H.
APPLICANT: Eisenberg, Roselyn J.
APPLICANT: Nicola, Anthony
TITLE OF INVENTION: Herpes Simplex Virus Glycoprotein D
TITLE OF INVENTION: Variants
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,568
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5654174and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-499-568-4

Query Match 8.2%; Score 190; DB 1; Length 394;
Best Local Similarity 23.2%; Pred. No. 2.9e-11;
Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;
QY 106 PYNRILTRSRGCDVLEINPISNVDMISAKEKEKGFPEASVYVFVITKGDGEDKIC 165
Db 79 PITYVAVLERACRSVLLNAPSEAPQIVRGASEDVAKQOYNLTIMFRM-----GNCAL 133
QY 166 PIYKREYREGCDVQLLSECAVQSAQMAVADYVPS--TLVSRNGAGLITFPTAALSGOYL 224
Db 134 PITYVAVLERACRSVLLNAPSEAPQIVRGASEDVAKQOYNLTIMFRM-----GNCAL 133
QY 225 TLKIGREFQATLVLE--VNDRCILKIGSQLNPLPSKCTTQYOTG-----FQG 271
Db 192 LKINDMTEI1QFLEHRAKSGC--KYALPLRIPSACLSPQAYOQGVTVDSIGMLPRFIP 250
QY 272 EHLVPIADNTNRHADDVYRGYEDILQRMNLLRKKNPSAPDRPDSVPOEIPAVTKKAEG 331
Db 251 ENQRTVAAYSLKLAG-----WH-----GPKAP-YTSTLLPEL-----S 283
QY 332 RTPDAESSEKRAPDESD--MQAEASGENPALPEDEDEVEDTEHDDPNSDPYNDMP 390
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QY 391 AVIPEETKSSNAVSMPIFAFVACAVALLVGLLW 426
Db 342 LI-----AGAVGSLIALALVIC-----GIVYW 363

RESULT 15
US-08-793-958-4
Sequence 4, Application US/08793958
Patent No. 5814486
GENERAL INFORMATION:
APPLICANT: Cohen, Gary H.
APPLICANT: Eisenberg, Roselyn J.
APPLICANT: Nicola, Anthony
TITLE OF INVENTION: Herpes Simplex Virus Glycoprotein D
TITLE OF INVENTION: Variants
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,958
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/499,568
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5814486and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-793-958-4

Query Match 8.2%; Score 190; DB 2; Length 394;
Best Local Similarity 23.2%; Pred. No. 2.9e-11;
Matches 78; Conservative 47; Mismatches 145; Indels 66; Gaps 14;
QY 106 PYNRILTRSRGCDVLEINPISNVDMISAKEKEKGFPEASVYVFVITKGDGEDKIC 165
Db 79 PITYVAVLERACRSVLLNAPSEAPQIVRGASEDVAKQOYNLTIMFRM-----GNCAL 133
QY 166 PIYKREYREGCDVQLLSECAVQSAQMAVADYVPS--TLVSRNGAGLITFPTAALSGOYL 224
Db 134 PITYVAVLERACRSVLLNAPSEAPQIVRGASEDVAKQOYNLTIMFRM-----GNCAL 133
QY 225 TLKIGREFQATLVLE--VNDRCILKIGSQLNPLPSKCTTQYOTG-----FQG 271
Db 192 LKINDMTEI1QFLEHRAKSGC--KYALPLRIPSACLSPQAYOQGVTVDSIGMLPRFIP 250
QY 272 EHLVPIADNTNRHADDVYRGYEDILQRMNLLRKKNPSAPDRPDSVPOEIPAVTKKAEG 331
Db 251 ENQRTVAAYSLKLAG-----WH-----GPKAP-YTSTLLPEL-----S 283
QY 332 RTPDAESSEKRAPDESD--MQAEASGENPALPEDEDEVEDTEHDDPNSDPYNDMP 390

Db 284 ETPNA--TOPELAPEDEDSALLEDPVGTVAPOIPPNWHIPSIQDAATPYHHPATPNNMG 341
QY 391 AVIPVEETKSSNAYSMPIFAAFYACAVALVGLLW 426
Db 342 LI-----AGAVGSSLALALVIC-----GIVYW 363

Search Completed: February 19, 2003, 16:23:55
Job time : 20 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2003, 16:23:39 ; Search time 13 Seconds

(Without alignments)
852.939 Million cell updates/sec

Title: US-09-994-064-11

Perfect score: 2311
Sequence: 1 MHRPHLRHRRHYAKGEVLN.....ACAAVGLVWSTVRCARS 434

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*
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2: /cgn2_6/ptodata/2/pubppaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2311	100.0	434	10	US-09-881-457A-4
2	117	5.1	311	10	US-09-883-720-16
3	115	5.0	1648	10	US-09-515-806-4
4	112.5	4.9	305	10	US-09-883-720-12
5	110.5	4.8	302	10	US-09-883-720-14
6	110.5	4.8	1643	10	US-09-515-806-2
7	103.5	4.5	764	9	US-09-854-133-67
8	103.5	4.5	764	10	US-09-738-973-67
9	103	4.5	258	10	US-09-765-272-90
10	103	4.5	365	10	US-09-765-272-218
11	103	4.5	26926	9	US-09-759-508B-2
12	101	4.4	285	10	US-09-883-720-18
13	97.5	4.2	300	10	US-09-919-770-2
14	97	4.2	428	9	US-09-906-514-4
15	95.5	4.1	2462	9	US-08-819-104A-5
16	95	4.1	897	10	US-09-815-242-12769
17	95	4.1	1113	10	US-09-815-242-5836
18	94.5	4.1	314	10	US-09-206-576-2
19	94.5	4.1	356	10	US-09-791-961-3

20	94.5	4.1	2507	9	US-09-819-104A-2	Sequence 2, App1
21	94	4.1	508	10	US-09-016-159-5	Sequence 5, App1
22	94	4.1	1162	9	US-10-079-625-43	Sequence 43, App1
23	94	4.1	1198	10	US-09-866-582-36	Sequence 36, App1
24	94	4.1	1241	12	US-10-001-215-5	Sequence 5, App1
25	94	4.1	2485	10	US-09-802-669-46	Sequence 46, App1
26	93	4.0	254	10	US-09-216-393-126	Sequence 126, App
27	92.5	4.0	472	9	US-09-738-626-6752	Sequence 6752, Ap
28	91.5	4.0	423	9	US-09-738-626-3778	Sequence 3778, Ap
29	91.5	4.0	603	10	US-09-764-868-705	Sequence 705, App
30	91.5	4.0	763	10	US-09-765-272-66	Sequence 66, App1
31	91	3.9	545	10	US-09-967-624-5	Sequence 5, App1
32	90.5	3.9	488	10	US-09-925-300-1563	Sequence 1563, Ap
33	90	3.9	489	10	US-09-817-913-3	Sequence 3, App1
34	90	3.9	489	10	US-09-817-538-3	Sequence 3, App1
35	90	3.9	576	10	US-09-347-331-11	Sequence 11, App1
36	90	3.9	590	10	US-09-925-300-1219	Sequence 1219, Ap
37	89	3.9	265	12	US-10-073-256-78	Sequence 78, App1
38	89	3.9	863	9	US-10-016-634A-141	Sequence 141, App
39	88.5	3.8	577	9	US-10-029-180-48	Sequence 48, App1
40	88.5	3.8	693	10	US-09-752-639-154	Sequence 154, App
41	88.5	3.8	693	10	US-09-984-198-154	Sequence 154, App
42	88	3.8	214	10	US-09-214-881A-1	Sequence 1, App1
43	88	3.8	481	10	US-09-817-913-1	Sequence 1, App1
44	88	3.8	481	10	US-09-817-538-1	Sequence 1, App1
45	87.5	3.8	236	9	US-10-174-550-544	Sequence 544, App

ALIGNMENTS

RESULT 1
US-09-881-457A-4
: Sequence 4, Application US/09881457A
: Patent No. US20020081316A1
: GENERAL INFORMATION:
: APPLICANT: Cochran, Mark D
: APPLICANT: Cook, Stephanie M
: TITLE OF INVENTION: Wild, Martha A
: FILE REFERENCE: SY01105K10KOK
: CURRENT APPLICATION NUMBER: US/09/881,457A
: CURRENT FILING DATE: 2001-06-14
: PRIOR APPLICATION NUMBER: 09/426,352
: PRIOR FILING DATE: 1999-10-25
: PRIOR APPLICATION NUMBER: 08/804,372
: PRIOR FILING DATE: 1997-02-21
: PRIOR APPLICATION NUMBER: PCT/US95/10245
: PRIOR FILING DATE: 1995-08-09
: PRIOR APPLICATION NUMBER: 08/663,566
: PRIOR FILING DATE: 1996-06-13
: PRIOR APPLICATION NUMBER: 08/288,065
: PRIOR FILING DATE: 1994-08-09
: PRIOR APPLICATION NUMBER: PCT/US93/05681
: PRIOR FILING DATE: 1993-06-14
: PRIOR APPLICATION NUMBER: 08/023,610
: PRIOR FILING DATE: 1993-02-26
: PRIOR APPLICATION NUMBER: 07/898,087
: PRIOR FILING DATE: 1992-06-12
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 434
: TYPE: PRT
: ORGANISM: Infectious Laryngotracheitis Virus
US-09-881-457A-4
Query Match 100.0%; Score 2311; DB 10; Length 434;
Best Local Similarity 100.0%; Pred. No. 2.5e-191;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MRPPIRRSRYYKAGEVLNKNHDCGKRCCGAAVLTFTWTCVRIMREHICFVNAMDR 60
Qy      61 HLELRNAFWTIVLLSSFASQSTAAVTYDYLGRRALDALTIPAVGPNRYLRRSGDY 120
Db      61 HLELRNAFWTIVLLSSFASQSTAAVTYDYLGRRALDALTIPAVGPNRYLRRSGDY 120
Qy      121 VELNPISNVDDMISAKEKEKGPPEASVYWFYVIKGGDEKDYCPYIRKEYRECGDYOL 180
Db      121 VELNPISNVDDMISAKEKEKGPPEASVYWFYVIKGGDEKDYCPYIRKEYRECGDYOL 180
Qy      181 ISECAVQASQMAVAVYVSTIVSRNAGLITFSPALSGOYLTLTKIGRAQTALVLE 240
Db      181 ISECAVQASQMAVAVYVSTIVSRNAGLITFSPALSGOYLTLTKIGRAQTALVLE 240
Qy      241 VNDRLCKIGSOLNLPKSCWTEQYOTGFQGEHLPIADTYRRAHDVYRGEDTLQWNN 300
Db      241 VNDRLCKIGSOLNLPKSCWTEQYOTGFQGEHLPIADTYRRAHDVYRGEDTLQWNN 300
Qy      301 NILRRKNPSADPPRDSVPQELPAVTKKAEGRTPDAESSEKKAPPEDEDDMOAASGEN 360
Db      301 NILRRKNPSADPPRDSVPQELPAVTKKAEGRTPDAESSEKKAPPEDEDDMOAASGEN 360
Qy      361 PAALPEDEVEDTEHDHPNSDPDYNDMPAVIPVEETTKSSNAVSMPIFAAFACAVAL 420
Db      361 PAALPEDEVEDTEHDHPNSDPDYNDMPAVIPVEETTKSSNAVSMPIFAAFACAVAL 420
Qy      421 VGLLWVSIVKCAR 434
Db      421 VGLLWVSIVKCAR 434

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RESULT 2

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US-09-883-720-16
; Sequence 16, Application US/09883720
; Patent No. US200202256A1
; GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
; FILE REFERENCE: 5718-44,
; CURRENT APPLICATION NUMBER: US/09/883,720
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/282,305
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Zea mays
US-09-883-720-16

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Query Match          5.1%; Score 117; DB 10; Length 311;
Best Local Similarity 22.8%; Pred. No. 0.016;
Matches 56; Conservative 39; Mismatches 103; Indels 48; Gaps 10;

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Qy      190 QMAVAVYVP-STIVSRNAGLITFSPALSGOYLTLTKIGRAQTALVLENDRLCKI 248
Db      2 EFWGLELVKPGSTVCKECPHGGLFHVSOAL-GE-----SKKSDSLMVKVDKRLAI 53
Qy      249 GS-----QLNF-----LPKSCWTEQYOTGFQGEHLPIADTYRRAHDVYRG 292
Db      54 GTLSIDIKYQIQIDLVFNKEFELSHSKTTSVFFSGIKVEQ--PI-----RGDEMDLDS 105
Qy      293 EDLQWNNLNLRRKNPSADPPRDSVPQELPAVTKKAEGRTPDAESSEKKA 343
Db      106 EDEEELNPIVYIKENKADGKEOKQKAVATAFSKSLGLEKSKSDSDSDSDSDSD 165
Qy      344 PEDSDMDQAASGENPALPEDEVEDTEHDHPNSDPDYNDMPAVIPVEETTKSSN 403
Db      166 SPEDSDSDSD-EGEGLSPDEGDDSDSDSDSDSDDEETP-----TPKKPEAGKRGAE 219

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Qy      404 AVSMPI 409
Db      220 ALKTP 225

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RESULT 3

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US-09-515-806-4
; Sequence 4, Application US/09515806
; Patent No. US20020132321A1
; GENERAL INFORMATION:
; APPLICANT: COOK, WILLIAM J.
; APPLICANT: KAPILLER-LIBERMAN, ROSANA
; TITLE OF INVENTION: 14790. NOVEL PROTEIN KINASE MOLECULE AND USES THEREFOR
; FILE REFERENCE: 38155-20002.00
; CURRENT APPLICATION NUMBER: US/09/515,806
; CURRENT FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1648
; TYPE: PRT
; ORGANISM: Murine Species
US-09-515-806-4

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Query Match          5.0%; Score 115; DB 10; Length 1648;
Best Local Similarity 22.6%; Pred. No. 0.24;
Matches 54; Conservative 31; Mismatches 98; Indels 56; Gaps 11;

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Db      558 DYIEIVIPSNQLPASAFSETQKQFSRYFIEEELQLLQKGFAGVAVIKQ----- 607
Qy      251 QNFPLKSCWTEQYOTGFQGEHLPIADTYRRAHDVYRGEDTLQWNNLRRK 306
Db      608 --NKIDGCCYAVKRIPIINPASFRRIRKEVILSRILHENTIVARY-----NAM--IERHE 659
Qy      307 NPSAP-DPPRDSVP--QELPAVTKKAEGRTPDAESSEKKAPPEDEDDMOAASGENPAA 363
Db      660 RPAVETPPPPDCTPQAQSDPATCGKTSGLTELGSYEAAPPIILSSVEMSTASERST 719
Qy      364 L-----PEDEVEDTEHD-----DPNSDPDYNDMPAVIPVEETTKSSN 403
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RESULT 4

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US-09-883-720-12
; Sequence 12, Application US/09883720
; Patent No. US200202256A1
; GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
; FILE REFERENCE: 5718-44,
; CURRENT APPLICATION NUMBER: US/09/883,720
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/282,305
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Zea mays
US-09-883-720-12

```

```

Query Match          4.9%; Score 112.5; DB 10; Length 305;
Best Local Similarity 23.1%; Pred. No. 0.038;
Matches 50; Conservative 43; Mismatches 80; Indels 43; Gaps 9;
Qy      190 QMAVAVYVP-STIVSRNAGLITFSPALSGOYLTLTKIGRAQTALVLENDRLCKI 248

```

```

Db      2  EFMGLEVKPGSTVACGEFGYGVLLSQAL-GE-----SKSDNMLMYVKIDDKLAI 53
Oy      249  GS-----QLNFLPSKCM-----TTEQYOTGQGEHLYPADTNRHADVRYG 292
           !: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      54  GTLSVDKNPIHQFLIDPEKEFLSHTSKTSVFETGYKVPQPF-----EEDMDLDS 105
           !: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      293  EDLIQRNNNLIRKKNPSAPDRPDSVQOETPAVYKAKDGRTPPAASESEKKAPEDSDDM 352
           !: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      106  EDEBEELNVPVVKKNGKADKKOKSOEKAAVAAPSKS-----SPDS---KSKDDDDSD 157
           !: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      353  QAEASGENPALPEDDEVPEDTEHDDDDNSPDYND 388
           !: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      158  ETDSDDEDET--DSDSEGLSEEDDDSDSDDEDPTSD 191
           !: : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

? RESULT 5
? US-09-883-720-14
? Sequence 14, Application US/09883720
? Patent No. US20020022256A1
? GENERAL INFORMATION:
? APPLICANT: Baldwin, Donald A.
? APPLICANT: Briggs, Steven P.
? APPLICANT: Crane, Virginia C.
? TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
? FILE REFERENCE: 5718-44.
? CURRENT APPLICATION NUMBER: US/09/883,720
? CURRENT FILING DATE: 2001-06-18
? PRIOR APPLICATION NUMBER: 09/282,305
? PRIOR FILING DATE: 1999-03-31
? NUMBER OF SEQ ID NOS: 18
? SOFTWARE: SeqEdit Ver. 2.0
? SEQ ID NO 14
? LENGTH: 302
? TYPE: PRT
? ORGANISM: Zea mays
? US-09-883-720-14

```

	Query Match	4.8%	Score 110.5;	DB 10;	Length 302;	
	Best Local Similarity	23.1%	Pred. No. 0.055;			
	Matches 50;	Conservative 42;	Mismatches 81;	Indels 43;	Gaps 9;	
QY	190 QMAVAVYP-STLVSRNAGLTITFSPRALSGOYLTLTKIGRFAGTALVTLEVNDRCLKI	248	:	:	:	:
	: : : :	: : : :	: : :	: : : : : :	: : :	:
Db	2 EFMGLEVPKGSSTVACEPGYGFVLHLSQAAL-GE-----SKSDNALMYIVKIDDKLAI	53	:	:	:	:
	: : : :	: : : :	: : :	: : : : : :	: : :	:
QY	249 GS-----QLNFPSCKM-----TTBYONGFOGHEHYPLADNTTRRADVDYRKY	292	:	:	:	:
	: : : :	: : : :	: : :	: : : : : :	: : :	:
Db	54 GLTVSDKKPPIHQFDLIPEKEFEISTSKTSKVTFEFGYKEOPF-----EEDEKDLDLS	105	:	:	:	:
	: : : :	: : : :	: : :	: : : : : :	: : :	:
QY	293 EDILQRNNMLLRKKNPASDPDRPDSVPOEIPATVKAKGRTPDAESSEKAPPESEDMD	352	:	:	:	:
	: : : : : :	: : : : : :	: : :	: : : : : :	: : :	:
Db	106 EEDEDELNVPVYKENGKADKKOKSOEKAVAPASKS----SPDS---KKSKDDDDSDDED	157	:	:	:	:
	: : : : : :	: : : : : :	: : :	: : : : : :	: : :	:
QY	353 QAELASGENPALPEDDEVPEDETENHPDPSDPYYND	388	:	:	:	:
	: : : : : :	: : : : : :	: : :	: : : : : :	: : :	:
Db	158 ETDDSDDEDET--DDSDGLSSSEEGDDSDSDSDEDDTSD	191	:	:	:	:
	: : : : : :	: : : : : :	: : :	: : : : : :	: : :	:

```

RESULT 6
US-09-515-806-2
? Sequence 2, Application US/09515806
? Patent No. US20020132321A1
? GENERAL INFORMATION:
? APPLICANT: COOK, WILLIAM J.
? APPLICANT: KAPLELLER-LIBERMANN, ROSANA
? TITLE OF INVENTION: 14790, NOVEL PROTEIN KINASE MOLECULE AND USES THEREFOR
? FILE REFERENCE: 38155-20002.00
? CURRENT APPLICATION NUMBER: US/09/515.806
? CURRENT FILING DATE: 2000-02-29
? NUMBER OF SEQ ID NOS: 32
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 2
? LENGTH: 1643

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-515-806-2

```

Query Match	4.8%;	Score 110.5;	DB 10;	Length 1643;
Best Local Similarity	19.2%;	Pred. No. 0.59;		
Matches 76;	Conservative 58;	Mismatches 133;	Indels 129;	Gaps 21.

QY	79	SOSIAAVYVYDYLICRRALDALTTIPAVGPYNYLTVRSRG	-DVELNPTISNDDMTSAA	136
Db	435	ABGYIKTI-DVISIKRLADI	-----CKEDVFBDTRVRFSDNAL-PY	473
QY	137	KEKEKGFPEASVYVFWYIKGDGEDKXCPIYKREYECGDY	-----QLLSE	1833
Db	474	KTKKKGDVWRIGLILLISLISG	-----QEGEYPTIPSDLPADPQELKK	518
QY	184	C-AVQSAOMMA	-----VDYVSTLYSRNKGAGLTTFSP	214
Db	519	CVCDDKCRMSRPOOLKHSFINPQPKMPLVEQSPEDSGGDYVETVYIPSRNRLPSAAFESE	578	
QY	215	TAAISGCVLTLK	-----IGRFAQTAALVTLLEVN-DRCLKISQNLNPLSKCMTWEOXYOTGF	269
Db	579	TORQFSRIFFEEELQILGKAFCAVAVIKVOKKLDGCCYAAKRIPIINFA	-----SKQFR-1	6333
QY	270	QGEHLPIADIINTRHADVYRGVEDIILQRMNNLIRKKRNPAP	-DPRDSVP--QELPAVT	326
Db	634	KGE-----VTLISRLHNEIIVAY	-----NAM--IRHHRPAGCPGPRPDSGLPKKDDRAAR	663
QY	327	KKABGRTPDAESSEKKAPREDSEDDMOAENSGEN	-----PALP--EDDEVPEDTEH--	376
Db	684	GQPAADTFGLDSVEAALAPRPIISSSVESWSTSGERSASARFAPATGCGSSDDEDEDDEHGC	7434	
QY	377	-----DDPNSDPOVYNDMPAVIPEETKSSN	403	
Db	744	VFQSQFLPQASDESDDIIFDNE	-----DENKSSQN	772

```

RESULT 7
US-09-854-133-67
? Sequence 67, Application US/09854133
? Publication No. US20020183499A1
? GENERAL INFORMATION:
? APPLICANT: Lodges, Michael J.
? APPLICANT: Mohamath, Raodoh
? APPLICANT: Henderson, Robert A.
? APPLICANT: Benson, Darin R.
? APPLICANT: Secrist, Heather
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
? TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
? FILE REFERENCE: 210121.475C10
? CURRENT APPLICATION NUMBER: US/09/854,133
? CURRENT FILING DATE: 2001-05-11
? NUMBER OF SEQ ID NOS: 735
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 67
? LENGTH: 764
? TYPE: PRF
? ORGANISM: Homo sapien
US-09-854-133-67

```

[illegible]


```
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 565 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-09-765-272-218

Query Match          4.5%; Score 103; DB 10; Length 565;
Best Local Similarity 24.8%; Pred. No. 0.59; Indels 40; Gaps 7;
Matches 38; Conservative 24; Mismatches 51;

QY 276 PIADNTRHADVDYRGYEDILQRMNNLLRKNPSADPRDPSVQETIPAV--TKKAGRT 333
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 98 PAESKVEQAGEPYAPRED-----EKAPVEPEKQPEA-PEEKAVEPTKQEST 146
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 334 PDASSKKAPPEDS-----EDMQAASGENPALPEDDEVPE 372
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 147 PDRAETVEPEKETVQMSIEQPKVETPAVEKQTEPEEKEVQAGE-PVAPREDDEQAP- 204
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 373 DTEHDDPNSDDYNDMPAVIPEETTKSSNAV 405
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 205 -TAPVEPEKQPEVEPEEKA--VEETPKPEDKI 233

RESULT 11
US-09-759-508B-2
; Sequence 2, Application US/09759508B
; Publication No. US20020182599A1
; GENERAL INFORMATION:
; APPLICANT: Fishman, Mark C.
; TITLE OF INVENTION: Methods for Diagnosing and Treating Heart Disease
; FILE REFERENCE: 00786/381002
; CURRENT APPLICATION NUMBER: US/09/759,508B
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,787
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 26926
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-508B-2

Query Match          4.5%; Score 103; DB 9; Length 26926;
Best Local Similarity 32.1%; Pred. No. 1.3e+02; Indels 16; Gaps 3;
Matches 25; Conservative 12; Mismatches 25;

QY 305 KKNPSADPRDPSVQETIPAVTKKAGRTPDASSSEKKAP-----PESEDDMQAE----- 355
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 4536 KPPPEPEPTPIAPVTVPVGVGKAEKAPKEPAKPGIKGVPKTSPTEERKKLR 4595
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 356 --ASGENPALPEDDEV 371
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 4596 PGSGGEKP-----PDEAP 4608

RESULT 12
US-09-883-720-18
; Sequence 18, Application US/09883720
; Patent No. US2002022256A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
; FILE REFERENCE: 5718-44,
; CURRENT APPLICATION NUMBER: US/09/883,720
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/282,305
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Zea mays
US-09-883-720-18

Query Match          4.4%; Score 101; DB 10; Length 285;
Best Local Similarity 22.0%; Pred. No. 0.34; Indels 42; Gaps 10;
Matches 46; Conservative 44; Mismatches 77;

QY 190 QMNAVDPSTLVS-RNAGLITFSPTALSGOYLTLTKIGRPAQTALVLEVNDRCLKT 248
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 2 EFMGEEVYKPGATVYSCVKGDGLVHLSQALG-----EKKASENAIVSVKIDDKLYL 54
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 249 GSQLNPLPSKCWITEQ-----YQTFQGEHLPIADNTRHADVDYRGYEDILQRM 299
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 55 GT-----LSVEKHPQISCGLVFDKDFELSH-----NKTASVFQCGKSPVPLF 98
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 300 NNLLRKNPSADPRDPSV--QETPAVTKKAGRT--PDASSSEKKAPPESEDDMQA 354
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 99 ES-DSGEDSDSEVEPLIIMQNNELIKISTAKVPVKVIGIONADETSSGDDDFDSDS 157
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 355 EASGENPALPEDEVPEDETE-HDDPNSD 382
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 158 EMSEDESS--DEDEVSSDTSDSGSE 184

RESULT 13
US-09-919-770-2
; Sequence 2, Application US/09919770
; Patent No. US20020048577A1
; GENERAL INFORMATION:
; APPLICANT: Bornstein, Paul
; APPLICANT: Kyriakides, Themis
; APPLICANT: Ratner, Buddy
; APPLICANT: Giachelli, Cecilia
; APPLICANT: Martinson, Laura
; APPLICANT: Scatena, Marta
; TITLE OF INVENTION: Methods and Devices to Modulate the Wound Response
; FILE REFERENCE: UOFW117618
; CURRENT APPLICATION NUMBER: US/09/919,770
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,071
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-919-770-2

Query Match          4.2%; Score 97.5; DB 10; Length 300;
Best Local Similarity 22.6%; Pred. No. 0.72; Indels 25; Gaps 5;
Matches 30; Conservative 19; Mismatches 59;

QY 278 ADNTRHADVDYRGYEDILQRMNNLLRKNPSADPRDPS---VQETIPAVTKKAGRT 334
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 22 ADSGSSEKQLYNKYPDAVTWLN-----PDPSQKONLLAPQTLPSKSNESHDDHD 72
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 335 DAESSEKKAPPESEDDMQAASGENPALPEDDEVPEDETHDDPNSD---PDYNDMPA 391
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
```


GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 25, 2003, 12:53:18 : Search time 2105 Seconds

(without alignments)
10040.432 Million cell updates/sec

Title: US-09-994-064-10

Perfect score: 1305
Sequence: 1 ATGCACCGTCCTCATCTCAG.....TAAATGCCGCGCTAGCTAA 1305

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estinu:*
4: em_estov:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_esthum:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_iny:*
20: em_gss_pln:*
21: em_gss_vtl:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41.4	3.2	958	17	CNS03PCF
2	41.2	3.2	669	12	BE776357
3	40.8	3.1	321	12	BG874723
4	40.8	3.1	529	17	AG876396
5	40.6	3.1	317	9	AA942788
6	40.2	3.1	212	9	AD12890

7	40.2	3.1	865	12	BG345158
8	40	3.1	688	12	BE521413
9	40	3.1	915	17	CNS0322R
10	40	3.1	1101	17	CNS00KR2
11	40	3.1	1137	11	AY106791
12	39.6	3.0	558	12	BF825826
13	39.6	3.0	567	10	AV896003
14	39.6	3.0	596	14	BP007281
15	39.6	3.0	637	10	AY901789
16	39.6	3.0	660	14	BP002281
17	39.6	3.0	713	10	AV897918
18	39.6	3.0	715	10	AV892667
19	39.6	3.0	716	10	AV896867
20	39.6	3.0	1046	17	AG073741
21	39.4	3.0	451	9	AA552908
22	39.4	3.0	530	13	BM155457
23	39.4	3.0	633	13	BM178622
24	39.4	3.0	677	13	BM161314
25	39.4	3.0	709	14	BQ840906
26	39.4	3.0	828	12	BG418286
27	39.2	3.0	1208	9	AL514927
28	39	3.0	333	9	AL828671
29	39	3.0	541	13	B1864958
30	39	3.0	577	9	AL721696
31	39	3.0	596	14	BQ470238
32	38.8	3.0	567	10	BE393657
33	38.8	3.0	925	17	CNS0091P
34	38.6	3.0	364	9	AL723670
35	38.6	3.0	581	10	AV675337
36	38.4	2.9	295	12	BE908072
37	38.4	2.9	464	12	BE799902
38	38.4	2.9	2037	11	AY108662
39	38.2	2.9	317	10	AW291911
40	38.2	2.9	443	14	BM994532
41	38.2	2.9	450	13	B1366211
42	38.2	2.9	478	13	B1356327
43	38.2	2.9	485	9	AA202831
44	38.2	2.9	492	10	BE510710
45	38.2	2.9	506	13	B1229580

ALIGNMENTS

RESULT 1
CNS03PCF/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

958 bp DNA linear GSS 17-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-ORI end of clone
044H14 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL254472.1 GI:7975484
GSS: genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 958)
Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wluecker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
2 (bases 1 to 958)
Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wluecker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished


```

RESULT 10
CNS000K2      1101 bp   DNA      linear   GSS 03-JUN-1999
LOCUS          Drosophila melanogaster genome survey sequence T7 end of BAC:
DEFINITION    BACR17F22 of RCT-98 library from Drosophila melanogaster (fruit
VERSION        AL077673
KEYWORDS      fly), genomic survey sequence.
ACCESSION     AL077673.1  GI:4957249
SOURCE        GSS.
ORGANISM      Drosophila melanogaster.
               Drosophila melanogaster.
               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
               Ephydroidea; Drosophilidae; Drosophila.
REFERENCE     Genoscope.
AUTHORS       Direct Submission
TITLE         Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL       BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
               - Web : www.genoscope.cns.fr)
               Determination of this BAC-end sequence was carried out as part of a
               collaboration with the Berkeley Drosophila Genome Project (BDGP).
               The BDGP is constructing a physical map of the Drosophila
               melanogaster genome using these BACs. For further information
               please see http://www.fruitfly.org The BDGP Drosophila
               melanogaster BAC library was prepared by Kazutoyo Osoegawa and
               Aaron Mamoser in Pieter de Jong's laboratory in the Department of
               Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
               NY. The library is named RCT-98 and was constructed by partial
               EcoRI digestion of Drosophila DNA provided by the BDGP from the
               isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
               P1 and EST libraries. A more detailed description of the library
               and how to order individual BAC clones, the entire library, or
               filters for hybridization from the BACPAC resource center can be
               found at http://BACPAC.med.buffalo.edu/drosophila_bac.htm.
FEATURES
  source
    1..1101
    /organism="Drosophila melanogaster"
    /db_xref="taxon:7227"
    /clone="BACR17F22"
    /clone.lib="RCT-98"
    /note="end : 77"

BASE COUNT   191 a    94 c    163 g    151 t    502 others
ORIGIN
Query Match      3.1%; Score 40; DB 17; Length 1101;
Best Local Similarity 10.0%; Pred. No. 4.8;
Matches 33; Conservative 154; Mismatches 144; Indels 0; Gaps 0;

QY 832 GCAGACCAATACAGACACGCGAGCATATCGGGATACGAAGATATTCGCAG 891
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 757 KAGMAMMAKAKAGMAMMAAAMAMAKBDMAKAMMMMMMMMMVMMGMMGKSHM 816
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 892 CGCTGATATTCGTGAGGAAAAGATCTTACGCGCCAGACCCCTGTCACATAGC 951
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 817 MGRKMGKTMGRKMNVMGMAKKNKMMAMMMMMMMKMKDKNNMKCTKCMKKKY 876
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 952 GTCCCGCAAGAATTCCTGCTAACAAGAAGCGGAAGCGGACCCCGGAGCAGAA 1011
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DB 877 MAMMMMAKMMHMKHMKHMKHMKHMKHMKHMKHMKHMKHMKHMKHMKHMKH 936
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QY 1012 AGCAGCGAAAAGAGCCCTCCAGAGAGTCCGAGAGCAGCATGACGAGAGCTTCT 1071
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DB 937 ASMAKDKMDGAGAMMGNCMGMGMMAGKMKMMMMGAGVAMGVTAGKMKMGTMAMA 996
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QY 1072 GGAGAAATCTCGCGCCCTCCGAGAGACAGCAAGTCCCGGAGACCCGAGCAGCAT 1131
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DB 997 KMAKMAKHAIVNMGHMMKMMVNAKMKMMKMMKMMKMMKMMKMMKMMKMMK 1056
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QY 1132 GATCAAACTCGATCTGATCTATTACAATG 1162
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DB 1057 MACMNMKHMAGKKKKMMVMMMKMMMYND 1087

RESULT 11
AY106791      1137 bp   mRNA      linear   HTC 25-MAY-2002
LOCUS          Zea mays PCO109680 mRNA sequence.
DEFINITION    AY106791
ACCESSION     AY106791
VERSION        AY106791.1  GI:21209869
KEYWORDS      Zea mays.
SOURCE        Zea mays.
ORGANISM      Zea mays.
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
               clade; Panicoidae; Andropogoneae; Zea.
REFERENCE     1 (bases 1 to 1137)
AUTHORS       Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
               Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE         Maize Mapping Project/Dupont Consensus Sequences for Design of
JOURNAL       Overgo Probes
               Unpublished (2002)
REFERENCE     2 (bases 1 to 1137)
AUTHORS       Coe,E.C.
TITLE         Direct Submission
JOURNAL       Submitted (25-APR-2002) Maize Mapping Project, University of
               Missouri, Columbia, MO 65211, USA
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    Library"
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    configs to seed Dupont contigs; this resource was
    assembled by Dupont as part of a collaboration for the
    overgo addressing of BACs in conjunction with the Maize
    Mapping Project"

BASE COUNT   209 a    398 c    360 g    161 t     9 others
ORIGIN
Query Match      3.1%; Score 40; DB 11; Length 1137;
Best Local Similarity 52.4%; Pred. No. 4.8;
Matches 88; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

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DB 657 ACCTCGACGACCAAGATGCGCGGAGCGCGCTGAGCGACCGCTGCGAGAGCCCGG 716
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RESULT 12
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LOCUS          MR2-HN0036-171100-002-e03 HN0036 Homo sapiens cDNA, mRNA sequence.
DEFINITION    BF825826
ACCESSION     BF825826.1  GI:12168527
VERSION        BF825826.1  GI:12168527
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE     1 (bases 1 to 558)
AUTHORS       Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

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/organism="Ciona intestinalis"
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BASE COUNT      182 a      115 c      182 g      117 t
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Pred. No. 4.3;
Matches 99; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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Db 319 CCAACTGAAAGATTAATCTCAGGAAGAGGAGGACCAAGAGGAGGAGAA 378
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QY 1027 GCCCTTCAGAAAGACTCGAGGAGGACGACATGCGAGGAGGAGGAGGAG 1086
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Db 439 GACGAGATATATGACGACGATGATGACGAGATGATGATGATGATGATGAT 498
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Db 499 GACGACGACGACGATGAC 516

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RESULT 15
AV901789/c      637 bp      mRNA      linear      EST 09-NOV-2001
LOCUS          AV901789 Nori Satoh unpublished cDNA library, young adult Ciona
DEFINITION     intestinalis cDNA clone rciad52h17 3', mRNA sequence.
ACCESSION      AV901789
VERSION        AV901789.1 GI:16890887
KEYWORDS       EST.
SOURCE         Ciona intestinalis.
ORGANISM       Ciona intestinalis.
                Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
                Phlebobranchia; Clonidae; Ciona.

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REFERENCE
AUTHORS        1 (bases 1 to 637)
TITLE          Satoh, N., Satou, Y., Kohara, Y. and Shin-I, T.
JOURNAL        Expressed genes in Ciona intestinalis
                Unpublished (2000)
COMMENT        Contact: Nori Satoh
                Department of Zoology
                Kyoto University
                Sakyo-Ku, Kyoto 606-8502, Japan
                Tel: 81-75-753-4081
                Fax: 81-75-705-1113
                Email: satoh@escidian.zool.kyoto-u.ac.jp.

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BASE COUNT      165 a      161 c      93 g      218 t
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Query Match
Best Local Similarity 3.0%; Score 39.6; DB 10; Length 637;
Pred. No. 4.5;
Matches 99; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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QY 967 CCCGCTGTACCAAGAAAGGAGGCGACCCCGGACCGAAGGAGGAGAAAGAG 1026

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Db 575 CCAACTGAAAGATTAATCTCAGGAAGAGGAGGAGGACCAAGAGGAGGAGAA 516
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QY 1027 GCCCTTCAGAAAGACTCGAGGAGGACGACATGCGAGGAGGAGGAGGAG 1086
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Db 515 GAAGAGGAAAGACGACGATGATGATGACGACGATGATGATGATGATGATGAT 456
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QY 1087 GCCCTCCCGAAGACGACGAGTCCCGGAGACACCGAGCAGCATATCCAACTCGAT 1146
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Db 455 GACGAGATATATGACGACGATGATGACGAGATGATGACGACGATGATGATGAT 396
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Db 395 GACGACGACGACGATGAC 378

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Search completed: February 25, 2003, 13:44:50
Job time : 2117 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2003, 13:06:38 ; Search time 63 Seconds

(without alignments)
6352.590 Million cell updates/sec

Title: US-09-994-064-10

Perfect score: 1305
Sequence: 1 ATGCACCGCTCTCATCTCAG.....TAAATCGCGCTAGCTAA 1305Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 862724

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents, NA: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1305	100.0	1305	2	US-08-484-575A-19
2	1305	100.0	1305	3	US-08-477-459-19
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4	1305	100.0	1305	3	US-08-486-414-19
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6	1305	100.0	1305	5	PCT-US94-02252A-19
7	1305	100.0	1305	5	PCT-US96-03916-10
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12	41.6	3.2	390	4	US-09-197-649-7
13	37.4	2.9	2277	1	US-08-676-967-2
14	37.4	2.9	2277	1	US-08-676-974-2
15	37.4	2.9	2277	2	US-09-098-487-2
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34	34.2	2.6	5063	1	US-08-185-432-1	Sequence 1, Appl1
35	33.4	2.6	1100	3	US-09-248-335-53	Sequence 53, Appl1
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37	32.8	2.5	2984	5	PCT-US93-00893-1	Sequence 1, Appl1
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40	32.8	2.5	3777	4	US-08-933-803A-15	Sequence 15, Appl1
41	32.6	2.5	6305	4	US-09-221-017B-256	Sequence 256, App
42	32.4	2.5	1476	4	US-09-434-288-12	Sequence 12, App
43	32.4	2.5	28804	2	US-08-592-874-1	Sequence 1, Appl1
44	32.4	2.5	28804	3	US-09-096-942-2	Sequence 2, Appl1
45	32.4	2.5	28804	3	US-09-096-867-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-484-575A-19
Sequence 19, Application US/08484575A
Patent No. 5923538
GENERAL INFORMATION:
APPLICANT: Mark D. Cochran and David E. Junker
TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,575A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0450
TELEFAX: (212)391-0525
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1305 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1305
US-08-484-575A-19
Query Match 100.0%; Score 1305; DB 2; Length 1305;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-08-477-459-19
? Sequence 19, Application US/08477459
? Patent No. 6001369
? GENERAL INFORMATION:
? APPLICANT: Mark D. Cochran
? TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses
? NUMBER OF SEQUENCES: 20
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: John P. White
? STREET: 1185 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: USA
? ZIP: 10036
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: Patent Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? FILING DATE: 07-JUN-1995
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: White Esq, John P
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 278-0400
? TELEFAX: (212) 391-0525
? INFORMATION FOR SEQ ID NO: 19:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1305 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1305
? US-08-477-459-19

Query Match 100.0%; Score 1305; DB 3; Length 1305;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 961 GAAATTCGCGCTGTACCAAGAAAGGGAAGGCGCACCCCGGACGCAAGAAAGACGAA 1020
Db 961 GAAATTCGCGCTGTACCAAGAAAGGGAAGGCGCACCCCGGACGCAAGAAAGACGAA 1020
QY 1021 AAGAAAGGCGCTTCAGAAAGCTCGGAGAGCAGATGCAAGGCTCTTGGAGAAAT 1080
Db 1021 AAGAAAGGCGCTTCAGAAAGCTCGGAGAGCAGATGCAAGGCTCTTGGAGAAAT 1080
QY 1081 CCGCGCGCGCTCCGGAAGAGCAGAAAGTCCCGAGGAGACCGAGACAGATATCCAAAC 1140
Db 1081 CCGCGCGCGCTCCGGAAGAGCAGAAAGTCCCGAGGAGACCGAGACAGATATCCAAAC 1140
QY 1141 TCGGATCTGACTATTACAAATGACATGCCGCGGTGATCCGCGTGAAGAGACTACTAAA 1200
Db 1141 TCGGATCTGACTATTACAAATGACATGCCGCGGTGATCCGCGTGAAGAGACTACTAAA 1200
QY 1201 AATTCTAATGCGCTTCATGCGCAATATTGCGGCGCTTGTAGCTGCGCGGTGCGGCTC 1260
Db 1201 AATTCTAATGCGCTTCATGCGCAATATTGCGGCGCTTGTAGCTGCGCGGTGCGGCTC 1260
QY 1261 GTGGGGCTACTGTTTGGAGCATGCTAAATGCGGCGGTAAGCTAA 1305
Db 1261 GTGGGGCTACTGTTTGGAGCATGCTAAATGCGGCGGTAAGCTAA 1305

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RESULT 4

```

US-08-486-414-19
; Sequence 19, Application US/0848641B
; Patent No. 6136318
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: Junker, David E.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES AND USES THEREOF
; FILE REFERENCE: 427/1D
; CURRENT APPLICATION NUMBER: US/08/486,414B
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 1305
; TYPE: DNA
; ORGANISM: Fowlpox virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(432)
US-08-486-414-19

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Query Match      100.0%; Score 1305; DB 3; Length 1305;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCACCGTCTCATCTCAGACGCGACCTGCGTCTACGGAAGAGAGGCTGTTAAC 60
Db 1 ATGCACCGTCTCATCTCAGACGCGACCTGCGTCTACGGAAGAGAGGCTGTTAAC 60
QY 61 AAACACATGATTTGGCGTGAAGAAAGCGTCTCAGGCGCAGCTGATTTACTCTTTTC 120
Db 61 AAACACATGATTTGGCGTGAAGAAAGCGTCTCAGGCGCAGCTGATTTACTCTTTTC 120
QY 121 TGGACTTGTCAGATATATGCGGGAGCATATCTGTTTATACGAAAGCTATGACCGC 180
Db 121 TGGACTTGTCAGATATATGCGGGAGCATATCTGTTTATACGAAAGCTATGACCGC 180
QY 181 CATTTATTTTGAAGAAATGCTTTTGTGACTATCTGACTGCTTTCTCTGCTGACGAG 240
Db 181 CATTTATTTTGAAGAAATGCTTTTGTGACTATCTGACTGCTTTCTCTGCTGACGAG 240
QY 241 AECACCGCGCGCTCAGTACGATTAATTTTAAAGGCGCTGAGCGGCTAAC 300
Db 241 AECACCGCGCGCTCAGTACGATTAATTTTAAAGGCGCTGAGCGGCTAAC 300
QY 301 ATACCGGCGGTTGGCGGATTAACGATTAACCTCACTAGGATTAAGAGGCTGACGTT 360
Db 301 ATACCGGCGGTTGGCGGATTAACGATTAACCTCACTAGGATTAAGAGGCTGACGTT 360
QY 361 GTGAGCTCAACCCGATTTCTAACGTGAGCAGATGATATGCGGCGCAAGAAAGAG 420
Db 361 GTGAGCTCAACCCGATTTCTAACGTGAGCAGATGATATGCGGCGCAAGAAAGAG 420
QY 421 AAGGGGGGCGCTTTCGAGGCGCTCGTGTCTGTTCTACGTGATTAAGGCGAGCAGCGC 480
Db 421 AAGGGGGGCGCTTTCGAGGCGCTCGTGTCTGTTCTACGTGATTAAGGCGAGCAGCGC 480
QY 481 GAGGACAGTACTGTCATCTATAGAAAAGAGACAGGGAATGCGGCGACGTAACATG 540
Db 481 GAGGACAGTACTGTCATCTATAGAAAAGAGACAGGGAATGCGGCGACGTAACATG 540
QY 541 CTATCTGAATGCGCGCTTCAATCTGACAGATGTGGCAGTGTGACTATGTTCTAGCACC 600
Db 541 CTATCTGAATGCGCGCTTCAATCTGACAGATGTGGCAGTGTGACTATGTTCTAGCACC 600
QY 601 CTGTATCGGGAATGGCGGGGAGCTACTATATCTCCCGCACTGCTGCGCTCTGCGC 660
Db 601 CTGTATCGGGAATGGCGGGGAGCTACTATATCTCCCGCACTGCTGCGCTCTGCGC 660
QY 661 CAATACTTGTGACCCCTGAAATCGGGAGATTGCGCAACAGCTCTGTAACCTAGAA 720
Db 661 CAATACTTGTGACCCCTGAAATCGGGAGATTGCGCAACAGCTCTGTAACCTAGAA 720

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QY	721	GTAAAGCATGCGCTGTTTAAAGATGGGGTCCGACGCTAACTTTTAAACGCTCGAAATGCTGG	780
Db	721	GTAAAGCATGCGCTGTTTAAAGATGGGGTCCGACGCTAACTTTTAAACGCTCGAAATGCTGG	780
QY	781	ACAACAGAACAGTATACACACTGATATTTCAGAGCGACACCTTTTATCCATCGCAGACACC	840
Db	781	ACAACAGAACAGTATACACACTGATATTTCAGAGCGACACCTTTTATCCATCGCAGACACC	840
QY	841	AATACAGCAGACGGGAGCAGCATATATGGGGGATACGAATATTTCTGACGCGTGGAAAT	900
Db	841	AATACAGCAGACGGGAGCAGCATATATGGGGGATACGAATATTTCTGACGCGTGGAAAT	900
QY	901	AATTTCGTCAGAGAAAAGAAATCTTAGCGCCGCGACACCTCTGTCAGATAGCTCCCGCAA	960
Db	901	AATTTCGTCAGAGAAAAGAAATCTTAGCGCCGCGACACCTCTGTCAGATAGCTCCCGCAA	960
QY	961	GAAATTCCTCCGCTATACCAAGAAAAGCGGAAGGGCGCACCCCGGAGAGCAAAAGCAGCGAA	1020
Db	961	GAAATTCCTCCGCTATACCAAGAAAAGCGGAAGGGCGCACCCCGGAGAGCAAAAGCAGCGAA	1020
QY	1021	AAGAAGGCCCTCCAGAAAGACTCGGAGAGCAGACATATGACAGAGAGGCTTCTGAGAAAAT	1080
Db	1021	AAGAAGGCCCTCCAGAAAGACTCGGAGAGCAGACATATGACAGAGAGGCTTCTGAGAAAAT	1080
QY	1081	CTGCGCCGCTCTCCCGGAAAGACGAGCAAGTCCCGGAGACACCGAGCAGCATGATCAAAAC	1140
Db	1081	CTGCGCCGCTCTCCCGGAAAGACGAGCAAGTCCCGGAGACACCGAGCAGCATGATCAAAAC	1140
QY	1141	TCGATCTCTGACTATTACAAATGACATGCGCCGCGCGATCCCGGTGAGAGAACTACTTAA	1200
Db	1141	TCGATCTCTGACTATTACAAATGACATGCGCCGCGCGATCCCGGTGAGAGAACTACTTAA	1200
QY	1201	AGTTCTTAATGCGCGCTCCATGCCATATTCGCGGGTCTGATAGCTTGGCGGTGCGCTC	1260
Db	1201	AGTTCTTAATGCGCGCTCCATGCCATATTCGCGGGTCTGATAGCTTGGCGGTGCGCTC	1260
QY	1261	GTGGGGCTACTGTTTGGAGCATCGTAAATTCGCGCGCTAGACTTAA	1305
Db	1261	GTGGGGCTACTGTTTGGAGCATCGTAAATTCGCGCGCTAGACTTAA	1305

RESULT 5
 PCT-US94-01826A-19
 : Sequence 19, Application PC/US9401826A
 : GENERAL INFORMATION:
 : APPLICANT: Syntro Corporation, et al.
 : TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and Uses Thereof
 : NUMBER OF SEQUENCES: 20
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: John P. White
 : STREET: 30 Rockefeller Plaza
 : CITY: New York
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10112
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentln Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: PCT/US94/01826A
 : FILING DATE: 28-FEB-1994
 : CLASSIFICATION:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: White Esq, John P
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (212)977-9550
 : TELEFAX: (212)664-0525
 : TELEX: 422523
 : INFORMATION FOR SEQ ID NO: 19:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1305 base pairs

	Query Match	100.0%	Score 1305;	DB 5;	Length 1305;	
	Best Local Similarity	100.0%	Pred. No. 0;			
	Matches 1305;	Conservative	0;	Mismatches	0;	Gaps
1	ATGCACCGTCTCCATCTCAGACGCGACATCGCTTACTACGCCAAGAGAGGTGCTTAAC					60
1	ATGCACCGTCTCCATCTCAGACGCGACATCGCTTACTACGCCAAGAGAGGTGCTTAAC					60
61	AAACACATGATGATGCGGTGAGAAACGGTGTCTCAGCGCAGCTGATTCACCTCTTTC					120
61	AAACACATGATGATGCGGTGAGAAACGGTGTCTCAGCGCAGCTGATTCACCTCTTTC					120
121	TGGACTTGTGTAGAGATTATGCGGGAGCATATCTGCTTGTACGCAACGCTATGACCGC					180
121	TGGACTTGTGTAGAGATTATGCGGGAGCATATCTGCTTGTACGCAACGCTATGACCGC					180
181	CATTTATTTTGTAGGAAATGCTTTTGGATATGATCTGCTTCTTCCCTGCTAGCCAG					240
181	CATTTATTTTGTAGGAAATGCTTTTGGATATGATCTGCTTCTTCCCTGCTAGCCAG					240
241	AGCACCGCCCGCGTCACGATGACATATTTAGCCGCTGCGCGCGCTGACGCGCTAAC					300
241	AGCACCGCCCGCGTCACGATGACATATTTAGCCGCTGCGCGCGCTGACGCGCTAAC					300
301	ATACCGCGGCTTGGCCCGTATTAACGATATCTTCACTAGGCTATCAAGAGCTGCGACGTT					360
301	ATACCGCGGCTTGGCCCGTATTAACGATATCTTCACTAGGCTATCAAGAGCTGCGACGTT					360
361	GTCCAGCTCAACCCGATTTCTAACGTGGAGCAATGATTCGGCGCGCCAAAGAAAAGAG					420
361	GTCCAGCTCAACCCGATTTCTAACGTGGAGCAATGATTCGGCGCGCCAAAGAAAAGAG					420
421	AAGGGGGGCCCTTTCGAGGCGCTCGCTGCTGTCTTACGTGATTAAGGGCGACGACGCG					480
421	AAGGGGGGCCCTTTCGAGGCGCTCGCTGCTGTCTTACGTGATTAAGGGCGACGACGCG					480
481	GAGGCAAGTACTGTCTCAATCTATAGAAAAGTACAGGGAATGTGGCAGCTACACG					540
481	GAGGCAAGTACTGTCTCAATCTATAGAAAAGTACAGGGAATGTGGCAGCTACACG					540
541	CTATCTGATGATGGCGGCTTCAATCTGACACAGATGTGGCGAGTGACATGTTCTTACGACC					600
541	CTATCTGATGATGGCGGCTTCAATCTGACACAGATGTGGCGAGTGACATGTTCTTACGACC					600
601	CTTGTATGCGCAAAATGCGGCGGAGCTGACTATATTTCTCCCACTGCTGCGCTCTGCG					660
601	CTTGTATGCGCAAAATGCGGCGGAGCTGACTATATTTCTCCCACTGCTGCGCTCTGCG					660
661	CAATCTGCTGACCCCTGAAAATCGGAGATTTGGCAAAACGCTCTGTACTAGAA					720
661	CAATCTGCTGACCCCTGAAAATCGGAGATTTGGCAAAACGCTCTGTACTAGAA					720
721	GTTTACGATGCGGTTTAAAGATGGGTCGCGCTTAACTTTTTCACCGTCAAAATGCTGG					780
721	GTTTACGATGCGGTTTAAAGATGGGTCGCGCTTAACTTTTTCACCGTCAAAATGCTGG					780
781	ACACAGAAAGATATCAGACTGATTTCAAGCGCAACACCTTATTCGATCGACAGAC					840
781	ACACAGAAAGATATCAGACTGATTTCAAGCGCAACACCTTATTCGATCGACAGAC					840
841	AATACGACACGCGGAGACGATATGCGGATACGAAGATATTCGACGCGTGAAT					900
841	AATACGACACGCGGAGACGATATGCGGATACGAAGATATTCGACGCGTGAAT					900

Db 841 AATACACACACGCGAGACGTATATCGGGGATACGAAGATATCTCAGCGCTGAAT 900
QY 901 AATTTGCTAGAGAAAAAATCTTAGCGCGACACCCGTCGATAGGTCCCGCAA 960
Db 901 AATTTGCTAGAGAAAAAATCTTAGCGCGACACCCGTCGATAGGTCCCGCAA 960
QY 961 GAAATTCCTGCTGTACCAAGAAAGCGAGAGGCGCACCCGAGACGCAAGAGCGAA 1020
Db 961 GAAATTCCTGCTGTACCAAGAAAGCGAGAGGCGCACCCGAGACGCAAGAGCGAA 1020
QY 1021 AAGAAAGCCCTCCGAGAGACGTCGAGAGACATGACGAGAGGCTTCTGAGAAAT 1080
Db 1021 AAGAAAGCCCTCCGAGAGACGTCGAGAGACATGACGAGAGGCTTCTGAGAAAT 1080
QY 1081 CCGTCCGCGCTCCCGAAGACGAGAGTCCCGAGACACCGACGACGATGATCCAAAC 1140
Db 1081 CCGTCCGCGCTCCCGAAGACGAGAGTCCCGAGACACCGACGACGATGATCCAAAC 1140
QY 1141 TCGGATCTGACTATATACATGACATGCCCCCGTATCCCGGTGAGAGAGACTATAA 1200
Db 1141 TCGGATCTGACTATATACATGACATGCCCCCGTATCCCGGTGAGAGAGACTATAA 1200
QY 1201 AGTTCTATGCGCTCTCATGCCATATTCGCGGCGTTGCGAGCTGCGGCGCTC 1260
Db 1201 AGTTCTATGCGCTCTCATGCCATATTCGCGGCGTTGCGAGCTGCGGCGCTC 1260
QY 1261 GTGGGGCTACTGTTTGGAGCATCTAAATGCGCGGTAGCTAA 1305
Db 1261 GTGGGGCTACTGTTTGGAGCATCTAAATGCGCGGTAGCTAA 1305

RESULT 6
PCT-US94-02252A-19
Sequence 19, Application PC/TUS9402252A
GENERAL INFORMATION:
APPLICANT: Syntro Corporation, et al.
TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02252A
FILING DATE: 28-FEB-1994

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1305 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1305
PCT-US94-02252A-19.

Query Match 100.0%; Score 1305; DB 5; Length 1305;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACCGCTCCTCATCTCAGACGGCACTCCGCTACTACCGCAAGAGAGGTGCTTAAC 60
Db 1 ATGACCGCTCCTCATCTCAGACGGCACTCCGCTACTACCGCAAGAGAGGTGCTTAAC 60
QY 61 AAACACATGATATGCGGTGAGAAAACGGTGTCTCAGGCGCACCTGTATCACTCTTTTC 120
Db 61 AAACACATGATATGCGGTGAGAAAACGGTGTCTCAGGCGCACCTGTATCACTCTTTTC 120
QY 121 TGGACTGTGTCCAGGATATATGCGGAGCATATGCTTTTACGCAACGCTATGACCGC 180
Db 121 TGGACTGTGTCCAGGATATATGCGGAGCATATGCTTTTACGCAACGCTATGACCGC 180
QY 181 CATTTATTTTGAAGAAATGCTTTTGGACTATGCTACTGCTTCTTCTGCTAGCCAG 240
Db 181 CATTTATTTTGAAGAAATGCTTTTGGACTATGCTACTGCTTCTTCTGCTAGCCAG 240
QY 241 AGCACGCGCGCTCACGTAAGCTAATTTAGCCGTCGCGCTCGACGCGCTAAC 300
Db 241 AGCACGCGCGCTCACGTAAGCTAATTTAGCCGTCGCGCTCGACGCGCTAAC 300
QY 301 ATACCGGCGGTGCGCGTATTAACAGATACCTCAATAGGATACAGAGGCTGCGACGT 360
Db 301 ATACCGGCGGTGCGCGTATTAACAGATACCTCAATAGGATACAGAGGCTGCGACGT 360
QY 361 GTGAGCTCAACCCGATTTCTTAAGTGAGAGCATATATGCGGCGCAAGAAAAAGAG 420
Db 361 GTGAGCTCAACCCGATTTCTTAAGTGAGAGCATATATGCGGCGCAAGAAAAAGAG 420
QY 421 AAGGGGGGCGCTTTCAGAGGCTCCGTCGCTGCTTACGTAATTAAGGCGACAGCGC 480
Db 421 AAGGGGGGCGCTTTCAGAGGCTCCGTCGCTGCTTACGTAATTAAGGCGACAGCGC 480
QY 481 GAGGACAACTACTGTCATATAGAAAAGATAGAGGAATGAGGAGCGCTACAAACG 540
Db 481 GAGGACAACTACTGTCATATAGAAAAGATAGAGGAATGAGGAGCGCTACAAACG 540
QY 541 CTATCTGAATGCGCGCTCAATCTGCACAGATGTGGGAGTGAGACTATGCTAGCAC 600
Db 541 CTATCTGAATGCGCGCTCAATCTGCACAGATGTGGGAGTGAGACTATGCTAGCAC 600
QY 601 CTGTATGCGGAATGCGCGGAGTCTGACTATATCTCCCGACGCTGCGCTCTGCGC 660
Db 601 CTGTATGCGGAATGCGCGGAGTCTGACTATATCTCCCGACGCTGCGCTCTGCGC 660
QY 661 CAATCTGCTGACCCCTGAAATCGGAGATTGGCGAAACGCTCTGTATCTGTAGAA 720
Db 661 CAATCTGCTGACCCCTGAAATCGGAGATTGGCGAAACGCTCTGTATCTGTAGAA 720
QY 721 GTTAACGATCGCTGTTTAAAGATCGGGTCGACGCTTAACTTTTACCGTCAAAATGCTGG 780
Db 721 GTTAACGATCGCTGTTTAAAGATCGGGTCGACGCTTAACTTTTACCGTCAAAATGCTGG 780
QY 781 ACAACAGAAAGTATCAGACGATTTCAAGCGCAACCTTTATCCGATGCGACAGACC 840
Db 781 ACAACAGAAAGTATCAGACGATTTCAAGCGCAACCTTTATCCGATGCGACAGACC 840
QY 841 AATACACGACACGCGAGACGATATGCGGGATACGAAGATATTCGACGCTGGAAT 900
Db 841 AATACACGACACGCGAGACGATATGCGGGATACGAAGATATTCGACGCTGGAAT 900
QY 901 AATTTGCTAGAGAAAAAATCTTAGCGCGCACACCTCTGTCAGATAGGCTCCGCAA 960
Db 901 AATTTGCTAGAGAAAAAATCTTAGCGCGCACACCTCTGTCAGATAGGCTCCGCAA 960
QY 961 GAAATTCCTGCTGTACCAAGAAAGCGAGAGGCGCACCCCGAGACGCAAGAGCGAA 1020
Db 961 GAAATTCCTGCTGTACCAAGAAAGCGAGAGGCGCACCCCGAGACGCAAGAGCGAA 1020

QY 1081 CTTGCCGCGCTCCCGAAGACGAGATGCCCGAGACACGAGACGATGATCCAAAC 1140
 Db 1081 CTTGCCGCGCTCCCGAAGACGAGATGCCCGAGACACGAGACGATGATCCAAAC 1140
 QY 1141 TCGATCTGATATATACATGACATGCGCGCGCTGATCCCGTGAGAGACTACTAA 1200
 Db 1141 TCGATCTGATATATACATGACATGCGCGCGCTGATCCCGTGAGAGACTACTAA 1200
 QY 1201 ACTTCAATGCGCTGTCATGCGCATATTCGCGGCTTCTGATGCTGCGGCTGCGCTC 1260
 Db 1201 ACTTCAATGCGCTGTCATGCGCATATTCGCGGCTTCTGATGCTGCGGCTGCGCTC 1260
 QY 1261 GTGGGGCTACGTGTTGGAGCATCGTAAATGCGCGCTAGCTAA 1305
 Db 1261 GTGGGGCTACGTGTTGGAGCATCGTAAATGCGCGCTAGCTAA 1305

RESULT 8
PCT-US96-03916-1

Sequence 1, Application PC/TUS9603916

GENERAL INFORMATION:

APPLICANT: Wild, Martha A.
 TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/03916
 FILING DATE: 23-MAR-1995
 CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/126,597
 FILING DATE: 24-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 39116-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 391-0525
 TELEFAX: (212) 278-0400

INFORMATION FOR SEQ. ID NO. 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 13473 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOHETICAL: NO
 FEATURE:

NAME/KEY: CDS
 LOCATION: 1059..2489
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 2575..4107
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 4113..4445
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 4609..5487
 FEATURE:

NAME/KEY: CDS
 LOCATION: 5697..8654
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 9874..10962
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 11159..12658
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 12665..13447
 PCT-US96-03916-1

Query Match 100.0%; Score 1305; DB 5; Length 13473;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACCGCTCTCATCTCAGACGCACTGCGTTACTACGCCGAAAGAGAGTGCTTAAC 60
 Db 8462 ATGACCGCTCTCATCTCAGACGCACTGCGTTACTACGCCGAAAGAGAGTGCTTAAC 8521
 QY 61 AAACACATGATGCGGTGAGAAACGGTGTGCTCAGCGCAGCTGATTCACCTTTTC 120
 Db 8522 AAACACATGATGCGGTGAGAAACGGTGTGCTCAGCGCAGCTGATTCACCTTTTC 8581
 QY 121 TGGACTTGTGTCAGATTTGCGGGAGCATATCTGTTTGTACGCAACGCTATGACCGC 180
 Db 8582 TGGACTTGTGTCAGATTTGCGGGAGCATATCTGTTTGTACGCAACGCTATGACCGC 8641
 QY 181 CATTATTTTGTAGAAATGTTTGTGACTATGTAATGCTTCTTCTGCTAGCCAG 240
 Db 8642 CATTATTTTGTAGAAATGTTTGTGACTATGTAATGCTTCTTCTGCTAGCCAG 8701
 QY 241 AGCACCGCGCGCTCAGTACGATCAATTTTAGCCGCGCGCTGACGCGCTAAC 300
 Db 8702 AGCACCGCGCGCTCAGTACGATCAATTTTAGCCGCGCGCTGACGCGCTAAC 8761
 QY 301 ATACCGCGGTGGCCGCTATACAGATACCTCCTAGAGGTTTCAAGAGCTGCGAGCTT 360
 Db 8762 ATACCGCGGTGGCCGCTATACAGATACCTCCTAGAGGTTTCAAGAGCTGCGAGCTT 8821
 QY 361 GTGAGCTTCMAACCGATTTCTAACGTGAGCAGCATGATATGCGCGCGCGCGCGCGCG 420
 Db 8822 GTGAGCTTCMAACCGATTTCTAACGTGAGCAGCATGATATGCGCGCGCGCGCGCGCG 8881
 QY 421 AAGGGGGCGCTTTGAGAGCGCTCCGCTGCTGCTTCTACGATTAAGGCGACGACGCG 480
 Db 8882 AAGGGGGCGCTTTGAGAGCGCTCCGCTGCTGCTTCTACGATTAAGGCGACGACGCG 8941
 QY 481 GAGGACAGTACTGTCATCTATAGAAAAGTACAGAGATGAGGAGGAGGTGCAACTG 540
 Db 8942 GAGGACAGTACTGTCATCTATAGAAAAGTACAGAGATGAGGAGGAGGTGCAACTG 9001
 QY 541 CTATCTGAATGCGCGCTTCAATCTGACAGATGTGGGACATGACTATGTTCTAGCAC 600
 Db 9002 CTATCTGAATGCGCGCTTCAATCTGACAGATGTGGGACATGACTATGTTCTAGCAC 9061
 QY 601 CTTGATGCGCAAAATGCGCGGAGCTGACATATTTCCCGCACTGCTGCTGCTGCGC 660
 Db 9062 CTTGATGCGCAAAATGCGCGGAGCTGACATATTTCCCGCACTGCTGCTGCTGCGC 9121
 QY 661 CAATACCTTGTGACCTGGAATGCGGAGATTTGCGCAACAGCTGCTGTAACCTAGAA 720
 Db 9122 CAATACCTTGTGACCTGGAATGCGGAGATTTGCGCAACAGCTGCTGTAACCTAGAA 9181
 QY 721 GTTAAGATGCGGTGTTAAAGATGCGGTGCGAGCTTAACCTTTTACCGTGAATGCTGG 780
 Db 9182 GTTAAGATGCGGTGTTAAAGATGCGGTGCGAGCTTAACCTTTTACCGTGAATGCTGG 9241
 QY 781 ACAACAGACAGTATCAGATGATTTCAAGGGGACACCTTATCGAGTCGAGACACC 840
 Db 9242 ACAACAGACAGTATCAGATGATTTCAAGGGGACACCTTATCGAGTCGAGACACC 9301

QY	841	AATACAGACACGGGACGACGATATTTCGGGGATACGAAGATATTTCGAGGCGTGGAT	900
Db	9302	AATACAGACACGGGACGACGATATTTCGGGGATACGAAGATATTTCGAGGCGTGGAT	9361
QY	901	AATTGCTGAGGAAAAAAGATCCTAGCGGCCAGACCTCTGTCAGATAGCCGTCCGGCA	960
Db	9362	AATTGCTGAGGAAAAAAGATCCTAGCGGCCAGACCTCTGTCAGATAGCCGTCCGGCA	9421
QY	961	GAATTTCCCGCTGTACCAAGAAAGCGGAAGGGCGCACCCCGGACGAGAAAGCAGCGAA	1020
Db	9422	GAATTTCCCGCTGTACCAAGAAAGCGGAAGGGCGCACCCCGGACGAGAAAGCAGCGAA	9481
QY	1021	AAGAGGCGCCCTCAGAGAAGCTCGGAGGAGCAGCATCAGGACAGAGGCTCTGGAGAAAT	1080
Db	9482	AAGAGGCGCCCTCAGAGAAGCTCGGAGGAGCAGCATCAGGACAGAGGCTCTGGAGAAAT	9541
QY	1081	CTGCGCGCCCTCCCCGAGACGACGAGAGTCCCCGAGGACACCGAGCAGCATGATCCAAAC	1140
Db	9542	CTGCGCGCCCTCCCCGAGAGCGACGAGAGTCCCCGAGGACACCGAGCAGCATGATCCAAAC	9601
QY	1141	TGCGATCCTGACTATTTCATATGACATGACCGCCGCGGTATCCCGGTGGAGAGACTACTAAA	1200
Db	9602	TGCGATCCTGACTATTTCATATGACATGACCGCCGCGGTATCCCGGTGGAGAGACTACTAAA	9661
QY	1201	AGTTCTAATGCCGTTCACATGCCCATATTTCGGGGCTTGTAAGCTGCAGCGGTCCGCGTC	1260
Db	9662	AGTTCTAATGCCGTTCACATGCCCATATTTCGGGGCTTGTAAGCTGCAGCGGTCCGCGTC	9721
QY	1261	GTGGGGCTACTGCTTGGAGACATCGTAAATAGCGCCGAGACTAA	1305
Db	9722	GTGGGGCTACTGCTTGGAGACATCGTAAATAGCGCCGAGACTAA	9766

RESULT 9
 PCT-US96-03916-59
 Sequence 59, Application PC/TUS9603916
 GENERAL INFORMATION:
 APPLICANT: Wild, Martha A.
 APPLICANT: Cochran, Mark D.
 TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
 TITLE OF INVENTION: AND USES THEREOF
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/03916
 FILING DATE: 23-MAR-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/126,597
 FILING DATE: 24-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 39116-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 INFORMATION FOR SEQ ID NO: 59:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18912 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

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Db	11098	ATGCACCGTCCATCTCAGACGCGACATCGCTTACTACGCGAAGAGAGGTGCTTAAAC	11157
QY	61	AAACACATGATATGGCGGTGGAAGAAACGCGTCTGCTCAGGCGCAGCTGTATTCACTCTTTTC	120
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QY	1261	GTGGGGCTACTGTTTGGAGCATCGTAAAAATCGCGCGTAGCTAA	1305
Db	12358	GTGGGGCTACTGTTTGGAGCATCGTAAAAATCGCGCGTAGCTAA	12402

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QY 1079 ATCTGCGCGCCCTCCGAGACGACGAAGTCCCGAGGACACCGACGATGATCCAA 1138
Db 707 AYGAYGAYGAYGAYGARGARGARGAGGCTNTTYGAYGARGAYGARGARGARGARA 766
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Db 767 AYATHGA 773

Search completed: February 25, 2003, 14:51:28
Job time : 114 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 25, 2003, 13:44:53 ; Search time 89 seconds
(without alignments)
8235.274 Million cell updates/sec

Title: US-09-994-064-10

Perfect score: 1305
Sequence: 1 ATGCACCGGCTCATCTCAG.....TAAAGCGCGCTACTTAA 1305

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 442118 segs, 280819700 residues

Total number of hits satisfying chosen parameters: 884236

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

Published Applications -NA:*
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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1305	100.0	3605	US-09-881-457A-3	Sequence 3, Appl1
2	41.6	3.2	390	US-09-790-399-7	Sequence 7, Appl1
3	34.6	2.7	863	US-09-974-300-5249	Sequence 5249, Ap
4	34.6	2.7	1191	US-09-842-987-1	Sequence 1, Appl1
5	34.4	2.6	68750	US-10-014-717-1	Sequence 1, Appl1
6	34.2	2.6	384	US-09-864-761-24106	Sequence 24106, A
7	34.2	2.6	455	US-09-864-761-25125	Sequence 25125, A
8	34.2	2.6	563	US-09-864-761-7383	Sequence 7383, Ap
9	34.2	2.6	586	US-09-864-761-8395	Sequence 8395, Ap
10	34.2	2.6	2481	US-09-894-998-35	Sequence 35, Appl1
11	34	2.6	1038	US-09-974-300-2209	Sequence 2209, Ap
12	33.6	2.6	438	US-09-938-842A-125	Sequence 125, App
13	33.6	2.6	678	US-09-770-149-358	Sequence 358, App
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15	33.2	2.5	7386	US-09-819-104A-6	Sequence 6, Appl1
16	33.2	2.5	8544	US-09-819-104A-4	Sequence 4, Appl1
17	32.6	2.5	672	US-09-833-381-697	Sequence 697, App
18	32.6	2.5	2349	US-10-087-110-5	Sequence 5, Appl1
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C 21	31.8	2.4	414	10	US-09-983-965-338	Sequence 338, App
C 22	31.8	2.4	1020	9	US-09-738-626-2136	Sequence 2136, Ap
C 23	31.8	2.4	1359	9	US-09-738-626-2135	Sequence 2135, Ap
C 24	31.8	2.4	1473	9	US-09-995-898A-3	Sequence 3, Appl1
C 25	31.8	2.4	1560	9	US-09-995-898A-28	Sequence 28, Appl1
C 26	31.8	2.4	1624	10	US-09-795-380-19	Sequence 19, Appl1
C 27	31.8	2.4	2898	10	US-09-834-975-868	Sequence 868, App
C 28	31.8	2.4	2898	10	US-09-834-975-865	Sequence 865, App
C 29	31.6	2.4	3309400	9	US-09-738-626-1	Sequence 1, Appl1
C 30	31.6	2.4	705	9	US-09-285-306-68	Sequence 68, Appl1
C 31	31.4	2.4	1234	10	US-09-925-502-1	Sequence 752, App
C 32	31.4	2.4	1485	10	US-09-925-300-752	Sequence 993, App
C 33	31.4	2.4	1560	9	US-09-738-626-993	Sequence 3, Appl1
C 34	31.4	2.4	1864	10	US-09-770-621-3	Sequence 349, App
C 35	31.4	2.4	2135	10	US-09-925-297-349	Sequence 3, Appl1
C 36	31.4	2.4	2145	10	US-09-925-502-3	Sequence 3340, Ap
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C 38	31.4	2.4	19334	10	US-09-764-865-1943	Sequence 1, Appl1
C 39	31.4	2.4	3309400	9	US-09-738-626-1	Sequence 4, Appl1
C 40	31.2	2.4	2820	10	US-09-924-855A-4	Sequence 7, Appl1
C 41	31.2	2.4	7367	9	US-10-024-632-7	Sequence 30, Appl1
C 42	31.2	2.4	13842	9	US-09-860-846-30	Sequence 30, Appl1
C 43	31.2	2.4	13842	10	US-09-861-289-30	Sequence 5, Appl1
C 44	31.2	2.4	36778	9	US-09-860-846-5	Sequence 5, Appl1
C 45	31.2	2.4	36778	10	US-09-861-289-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-09-881-457A-3
Sequence 3, Application US/09881457A
Patent No. US20020081316A1
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Cook, Stephanie M
APPLICANT: Wild, Martha A
TITLE OF INVENTION: NO. US20020081316A1e1 Avian Herpes Virus and Uses Thereof
FILE REFERENCE: SY0110510XOK
CURRENT APPLICATION NUMBER: US/09/881,457A
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 09/426,352
PRIOR FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/804,372
PRIOR FILING DATE: 1997-02-21
PRIOR APPLICATION NUMBER: PCT/US95/10245
PRIOR FILING DATE: 1995-08-09
PRIOR APPLICATION NUMBER: 08/663,566
PRIOR FILING DATE: 1996-06-13
PRIOR APPLICATION NUMBER: 08/288,065
PRIOR FILING DATE: 1994-08-09
PRIOR APPLICATION NUMBER: PCT/US93/05681
PRIOR FILING DATE: 1993-06-14
PRIOR APPLICATION NUMBER: 08/023,610
PRIOR FILING DATE: 1993-02-26
PRIOR APPLICATION NUMBER: 07/898,087
PRIOR FILING DATE: 1992-06-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 3605
TYPE: DNA
ORGANISM: Infectious Laryngotracheitis Virus
FEATURE:
NAME/KEY: CDS
LOCATION: (585)..(1889)
OTHER INFORMATION: ILTV glycoprotein D
NAME/KEY: CDS
LOCATION: (1977)..(3085)
OTHER INFORMATION: ILTV glycoprotein I
US-09-881-457A-3

Query Match 100.0%; Score 1305; DB 10; Length 3605;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 645 AACACATGATGTCGGGTGGAACGGGTCGTCAGGCGAGTGTATTCACCTTTTC 704
QY 121 TGGACCTGTGTAGAGATTTATCGGAGACATATCTGCTTTGACGCAAGCTATGAGCCG 180
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DB 765 CATTTATTTTGGAGATGCTTTTGGACATGCTACTGCTTCTTCTTCCGTAGCCAG 824
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DB 825 AGCACCGCCCGCTCAGCTACGACTATTTAGCGCGCGCGCGCGCGCGCTTACC 884
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DB 1305 GTTAAAGATCGCTGTTTAAAGATCGGAGTTCGAGCTTAATTTTACCGCGGAATGCG 1364
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QY 1141 TCGGATCTGACATTAATTAATGACATGACATGACATGACATGACATGACATGAC 1200
DB 1725 TCGGATCTGACATTAATTAATGACATGACATGACATGACATGACATGACATGAC 1784
QY 1201 AGTTTAATGCGGTCACATGACATGACATGACATGACATGACATGACATGACATG 1260
DB 1785 AGTTTAATGCGGTCACATGACATGACATGACATGACATGACATGACATGACATG 1844
QY 1261 GTGGGGCTACTGTTTGGAGCATGTAATATGCGCGCTGAGCTAA 1305
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RESULT 2

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US-09-790-399-7
; Sequence 7, Application US/09790399
; Patent No. US20020038000A1
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Tuerk, Craig
; APPLICANT: Pribnow, David
; APPLICANT: Smith, Jonathan D.
; TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
; FILE REFERENCE: NEX02/CI-COM2
; CURRENT APPLICATION NUMBER: US/09/790,399
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/197,649
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: 07/829,461
; PRIOR FILING DATE: 1992-01-31
; PRIOR APPLICATION NUMBER: 07/739,055
; PRIOR FILING DATE: 1991-08-01
; PRIOR APPLICATION NUMBER: 07/561,968
; PRIOR FILING DATE: 1990-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO 7
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence
; OTHER INFORMATION: having a 120 repeat of AGC flanked by fixed
; OTHER INFORMATION: fragments having NcoI restriction sites.
US-09-790-399-7
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Query Match 3.2%; Score 41.6; DB 10; Length 390;
Best Local Similarity 51.6%; Pred. No. 0.0014;
Matches 95; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

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QY 1063 GAGGCTTCTGAGAAATCCGCGCCCTCCCGAAGACGAGCAAGTCCCGAGGACAC 1122
DB 261 GAGGCTTCTGAGAAATCCGCGCCCTCCCGAAGACGAGCAAGTCCCGAGGACAC 320
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QY 1183 GTGG 1186
DB 381 ATGG 384
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RESULT 3
US-09-974-300-5249
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: Patent No. US20020146721A1
: GENERAL INFORMATION:
: APPLICANT: Berka, Randy M.
: APPLICANT: Clausen, Ib Groth
: TITLE OF INVENTION: Methods For Monitoring Multiple Gene
: TITLE OF INVENTION: Expression
: FILE REFERENCE: 10085,500-US
: CURRENT APPLICATION NUMBER: US/09/974,300
: CURRENT FILING DATE: 2001-10-05
: PRIOR APPLICATION NUMBER: 09/680,598
: PRIOR FILING DATE: 2000-10-06
: PRIOR APPLICATION NUMBER: 60/279,526
: PRIOR FILING DATE: 2001-03-27
: NUMBER OF SEQ ID NOS: 8481
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5249
: LENGTH: 863
: TYPE: DNA
: ORGANISM: Bacillus clausii
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(863)
: OTHER INFORMATION: n = A,T,C or G
US-09-974-300-5249

Query Match 2.7%; Score 34.6; DB 10; Length 863;
Best local similarity 45.7%; Pred. No. 0.48;
Matches 121; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

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QY 992 GCGCCAGCCCGGAGCGCAGCAAGAGCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1051
Db 122 CGGAGCCCGATGCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATG 181
QY 1052 ACATGACGAGCAGAGAGCTTCTGAGAAATTCCTGCCGCCCTCCCGAAGCAGCAAGTCC 1111
Db 182 CCGAGCGAGAGCGGAGCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATG 241
QY 1112 CCGAGGACACGAGCAGCAGCATGATCCAACTCGGATCGGATCGGATCGGATCGGATG 1171
Db 242 CGGAGCGCGGAGCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATG 301
QY 1172 CCGTGAATCCCGTGAAGAGAGACTAC 1196
Db 302 CGGATCGCGAGCGGAGCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATG 326

RESULT 4
US-09-842-987-1
: Sequence 1, Application US/09842987
: Patent No. US2002025566A1
: GENERAL INFORMATION:
: APPLICANT: Bristol-Myers Squibb Company
: TITLE OF INVENTION: ENZYMATIC OXIDATIVE DEAMINATION PROCESS
: FILE REFERENCE: HA690
: CURRENT APPLICATION NUMBER: US/09/842,987
: CURRENT FILING DATE: 2001-04-26
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1
: LENGTH: 1191
: TYPE: DNA
: ORGANISM: Spingomonas paucimobillis
: US-09-842-987-1

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Query Match	Score	DB	Length
Query Match Similarity	49.2%	Pred. No. 0.58:	
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QY	934	GACCTCGTCCAGATAGCGTCCCGCAGAGAAATTCGCGCTGTAAACCAAGAAACGGAGAGG	993
Db	685	GCCCATGAACAATATGCGCGTGCAGCCGCGACATCATATGGCGGTGGCCAAAGGCGATCGGCGG	744
QY	994	CGCACCCCGGAGCGCAGAAAGACAGCCAAAAGAGGCCCTCCAGAAAGACTTCGGAGAGCAGC	1053
Db	745	GCGCTTCGCGCTCGGCGCGCTCGCTCCCTACCGAGATGCGGCCCAAGGCGATGGTGTTCGGC	804
QY	1054	ATCGAGCGAGAGCGCTTCGTGAGAAAATCCGCGCGCCCTCCCGCAGAGACGAGAGTCCCC	1113
Db	805	ACCCATGGTTCACCATATGCGCGCAACCCGCTCGCCATGCGGTGGGATCGCGGTCTG	864
QY	1114	GAGGA	1118
Db	865	GAGGA	869
RESULT 5			
US-10-014-717-1			
Sequence 1, Application US/10014717			
Publication No. US20020192778A1			
GENERAL INFORMATION:			
APPLICANT: Schnupp, Thomas			
APPLICANT: Ligon, James			
APPLICANT: Molnar, Istvan			
APPLICANT: Zikler, Ross			
APPLICANT: Cyr, Devon			
APPLICANT: Goelach, Joern			
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES			
FILE REFERENCE: 4-30582A			
CURRENT APPLICATION NUMBER: US/10/014.717			
CURRENT FILING DATE: 2001-11-13			
PRIOR APPLICATION NUMBER: US/09/335.409			
PRIOR FILING DATE: 1999-06-17			
NUMBER OF SEQ ID NOS: 30			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO 1			
LENGTH: 68750			
TYPE: DNA			
ORGANISM: Sorangium cellulosum			
US-10-014-717-1			
Query Match	2.6%	Score 34.4:	DB 9: Length 68750:
Best Local Similarity	46.3%	Pred. No. 8:	
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QY	275	GCCGTCGCGCGCTCGACGCGCTAACCATACGCGCGGTGTGCGCGTATACAGATACCTCA	334
Db	4433	GCGGCGCTAGGCGGCGAGGCGCGCGCTCGTGGCGGTGCGCTGAACATGAAGGCGGCA	4492
QY	335	CTAGGCTTCAAGAGGCTGCGAGCTTGTGAGACTCAACCCGATTTCTTAACGTGAGAGACA	394
Db	4493	GCGACCTATGCTGCGGATCGTCGCGGCTGCGAGCTCGGCGTCTCTTCACAGAGGCTTATA	4552
QY	395	TGATATCGCGCGCCAAAGAAAAGAGAGGCGGCGCTTTGAGAGGCTTCGTCGTGCT	454
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QY	455	TCTA	458
Db	4613	TCTA	4616
RESULT 6			
US-09-864-761-24106			

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: Sequence 24106, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharron G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: FILE REFERENCE: Aecomica-X-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263,6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 24106
: LENGTH: 384
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AL121988.10
: OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 2.6
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.4
: OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3
: OTHER INFORMATION: NT HIT: AF099731.1, EVALUE 0.00e+00
: OTHER INFORMATION: EST_HUMAN HIT: BE712515.1, EVALUE 0.00e+00
: OTHER INFORMATION: SWISSPROT HIT: O95377, EVALUE 3.00e-73
: US-09-864-761-24106

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QY 1048 GACGCAATCGAGCACAAGGCTTCTGSAAAAATCCGCCCTCCCGGCAAGCACGCAA 1107
||| ||| | | | | | | | | | | | | | |
Db 139 GACCACAGGAGGAGCATATTATTTGGGTGAATGATGTAACAATAAGAAAGCCGAT 198

QY 1108 GTCCCCAGAGACACCAGCAGCATGATCCAACTCGATCTGACTATTACAAATGACATG 1167
|||| | | | | | | | | | | | | | |
Db 199 GTGCACAGCTGCGCTTGAAACACTAGGCTGCAGACATATGTCCACAGAGCCCAACCCCGCTT 258

QY 1168 CCCGCGGTATCCCGTGTGAGGAGACTACTAAAAGTTCTAATGCCGTCATGCCCATTA 1227
- | | | | | | | | | | | | | | | | | |
Db 259 CTTGGCGGGGTTTCAGGTAGAAGGCGCCCACTGTTTCCCACATGGGCTTCTCGGTCCTTT 318

QY 1228 TTC 1230
||
Db 319 CTC 321

RESULT 7
US-09-864-761-25125
; Sequence 25125, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aesomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 25125
LENGTH: 455
TYPE: DNA
ORGANISM: Homo sapiens


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; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 8395
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL122010.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
US-09-864-761-8395

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Query Match
Best Local Similarity 2.6%; Score 34.2; DB 10; Length 586;
Matches 90; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

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QY 1048 GAGGACATGAGGACGAGGCTTGTGAGAAATCCTGCCCTCCCGAAGAGAGAGAA 1107
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DB 341 GAGGACAGGAGGAGAGATATTTGGGTGAGATGAGTGAACATAGAGAAAGCGCAT 400
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1108 GTCCCGGAGGACACGACGATGATCCAACTCGATCCGATCATATTAATGACANG 1167
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 401 GTCCACGCTCGCTTGAACACTGAGCTGACAGACATATGTCCACCAAGGCCCGCGTT 460
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1168 CCGGCGGTGATCCGCTGAGAGAGACTACTAAAGTTCTAATGCCCTCTCCATGCCCAT 1227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 461 CTGCGCGGGTTCAGTAGAGGCGCCACTGTCTCCCATGGGCTTCTCGGTGCTCTT 520
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1228 TTC 1230
    ||
DB 521 CTC 523

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RESULT 10
US-09-894-998-35/c
; Sequence 35, Application US/09894998
; Patent No. US2002090610A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Hosken, Nancy Ann
; APPLICANT: Craig H. Day
; APPLICANT: Davin C. Dillon
; APPLICANT: McGowan, Patrick
; APPLICANT: Sleath, Paul R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: 210121.538
; CURRENT APPLICATION NUMBER: US/09/894,998
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 2481
; TYPE: DNA
; ORGANISM: HSV-2
US-09-894-998-35

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Query Match
Best Local Similarity 48.2%; Score 34.2; DB 10; Length 2481;
Matches 96; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

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QY 927 CGGCGCAGACCTCTGTCAGATAGCGTCCGCAAGAAATTCGCTTAACCAAGAAAGC 986
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1902 CCCACACAGCCCCCGCCAGAGAGAGAGCGGAGAGAGAGCGAGAGAGAGAGAGG 1843
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 987 GGAAGGCGCACCCCGGAGCCAGAAAGCAAGCAGAAAGAGCCCTCCAGAAAGACTCGA 1046
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1842 GGAAGAGAGAGAGAGAGCGGAGAGAGAGAGAGCGGAGAGAGAGAGAGAGAGC 1783
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1047 GAGCAGATGACAGAGAGGCTTCTGAGAAATCCTGCCCTCCCGAAGAGAGAGCA 1106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1782 GAGAGAGAGAGAGAGCGGCGGCGAGCCGCGCTGTGAGACAGAGAGAGAGAGAGG 1723
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1107 AGTCCCCGAGAGACCGGAG 1125
    ||| ||| ||| ||| |||
DB 1722 GGGCGCCGGGAGCGCGG 1704
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RESULT 11
US-09-974-300-2209
; Sequence 2209, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, JB Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2209
; LENGTH: 1038
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2209

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```

Query Match
Best Local Similarity 2.6%; Score 34; DB 10; Length 1038;
Matches 88; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

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QY 994 GGCACCCGGAGCGAGAAAGAGAGAGCCCTCCAGAGACTCGAGAGAGAGC 1053
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DB 783 GCGTCTGTCTGTCAGAGAGAGAGAGAGAGTGTCTTACAAAAGAGAGAGAGAGTT 842
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1054 ATGACGAGAGAGGCTTCTGAGAAATCTCGCGCCCTCCCGAAGAGAGAGAGTCCC 1113
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 843 TCCGTGAGAGGTATGAGTACTCGCCGCAAAATCGGTGATGCGAGAAAAAGATGCC 902
QY 1114 GAGACACCCAGCAGCATGATCCAAATCTGCTACTCTATTCATGATGATGCCG 1171
Db 903 GCCAACCTTGTACATGCCAACAAACCGGAGATCTTGTCTATTCATTATATCATCCG 960

RESULT 12

US-09-938-842A-125
; Sequence 125, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIORITY FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 125
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-125

Query Match 2.6%; Score 33.6; DB 9; Length 438;
Best Local Similarity 52.1%; Pred. No. 0.69;

Matches 75; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1002 GGACGCAAGAAAGCAGAAAGAGCCCTCCAGAACTCGGAGAGCATGACAGCC 1061
Db 265 GGGAGGAGGTACCAAGAGAGGAGGAGCATACCAAGAGAGCGGTGGCGCAAGAGAGA 324
QY 1062 AGAGGCTTTGGAGAAATCTCGCCGCCGCCGAGAGAGAGCAATGCCCGAGAGAC 1121
Db 325 GGGGGAAGTGGGGAACTTCTGCCCGCAGCGCTGCTACAGAGGTTACAGCGCTGC 384
QY 1122 CGAGCAGATGATCCAAACTCGA 1145
Db 385 TCAAGATGCTGCTGTATGCCGA 408

RESULT 13

US-09-770-149-358/C
; Sequence 358, Application US/09770149
; Patent No. US2002005963A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Moessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith

; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; PRIORITY FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 358
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-149-358

Query Match 2.6%; Score 33.6; DB 10; Length 678;
Best Local Similarity 52.1%; Pred. No. 0.89;

Matches 75; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1002 GGACGCAAGAAAGCAGAAAGAGCCCTCCAGAACTCGGAGAGCATGACAGCC 1061
Db 403 GGGAGGAGGTACCAAGAGAGGAGGAGCATACCAAGAGAGCGGTGGCGCAAGAGAGA 344
QY 1062 AGAGGCTTTGGAGAAATCTCGCCGCCGCCGAGAGAGCAGCAATGCCCGAGAGAC 1121
Db 343 GGGGGAAGTGGGGAACTTCTGCCCGCAGCGCTGCTACAGAGGTTACAGCGCTGC 284
QY 1122 CGAGCAGATGATCCAAACTCGA 1145
Db 283 TCAAGATGCTGCTGTATGCCGA 260

RESULT 14

US-09-938-842A-1892/C
; Sequence 1892, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIORITY FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1892
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1892

Query Match 2.6%; Score 33.6; DB 9; Length 1503;
Best Local Similarity 57.7%; Pred. No. 1.4;

Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 890 AGCCGTGAATTAATTTCTAGAGAAAGATCTACGCGCGAGACCTCGTCCACATA 949
Db 388 ATGCTTCAAGTAAGCCCAAGCATGTGACAATTTCTGCTCCAAAGCTTGTCCACATA 329
QY 950 GCGTCCGCAAGAAATTCGCGTGTACCAAGAAAGCGGAGG 993
Db 328 GCGTTTCAAGCACTTCCATTCCAGCATGATGCCGATGAG 285

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RESULT 15
US-09-819-104A-6
; Sequence 6, Application US/09819104A
; Publication No. US20030027137A1
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; PRIOR APPLICATION NUMBER: 2001-03-27
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 7386
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(7386)
US-09-819-104A-6

Query Match      2.5%; Score 33.2; DB 9; Length 7386;
Best Local Similarity 52.1%; Pred. No. 5.2;
Matches 74; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 997 ACCCCGAGCGAAGAAAGCAGAGAGCCCTCCAGAGACTCGAGAGACATG 1056
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2044 ACCCCAGCTGCGGCGAGCGAGACAGCCTTCCACCTCGCTGAGAGAGATG 2103
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1057 CAGGCGAGAGCTTCTGAGAGAAATCTGCCGCCCTCCCGAGAGCGAAGTCCCGAG 1116
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2104 GAAGCATCAGGCGCAAGTGCCATGAGAGAGACTGGCGGAGAGCGAGAGCCTCACAG 2163
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1117 GACACCGAGCGATGATCCAA 1138
    ||||| ||||| ||||| |||||
Db 2164 GCCTCTGGGAATGAGTTCCCA 2185
    ||||| ||||| ||||| |||||
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Job time : 108 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2003, 12:53:59 ; Search time 3584 seconds

(without alignments)
10596.864 Million cell updates/sec

Title: US-09-994-064-10

Sequence: 1 ATGCACCGTCCTCATCTCAG.....TAAATGCGCGGTAGCTAA 1305

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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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1	1305	100.0	1305	6	AR093367	AR093367 Sequence
2	1305	100.0	1305	6	AR135449	AR135449 Sequence
3	1305	100.0	18912	14	ILUW8832	U28832 Infectious
4	1268.2	97.2	1627	14	HSMGGLYCO	L11965 Gallid herp
5	361	27.7	3502	6	A22122	A22122 ITfV gp60 g
6	52.2	4.0	161046	14	AF081810	AF081810 Lymntria
7	45.8	3.5	2676	1	MAFAPD	M33247 M.xanthus s
8	45.8	3.5	7980	1	MXU20669	U20669 Myxococcus
9	44.4	3.4	7218	8	166494	I66494 Sequence 14
10	44.4	3.4	185863	2	AC121079	AC121079 Mus muscu
11	43.6	3.3	99360	8	NCB11N2	AL5131409 Mus muscu
12	43.4	3.3	125020	8	AF429315	AF429315 Homo sapi
13	43	3.3	3022	8	SCYOR053W	Z74961 S.cerevisia
14	43	3.3	54719	8	SCXSV5KB	Z70678 S.cerevisia
15	42.8	3.3	202761	2	AC104329	AC104329 Mus muscu
16	41.8	3.2	181003	2	AC127549	AC127549 Mus muscu
17	41.6	3.2	181931	2	AC115847	AC115847 Mus muscu
18	41.6	3.2	390	6	AR135147	AR135147 Sequence
19	41.4	3.2	149333	2	AF004592	AF004592 Oryza sat
20	41.2	3.2	191584	2	AC120477	AC120477 Rattus no
21	41	3.1	67392	2	AC110550	AC110550 Mus muscu
22	40.8	3.1	187466	2	AC102480	AC102480 Mus muscu
23	40.6	3.1	158955	2	AC115344	AC115344 Rattus no
24	40.4	3.1	158531	2	AC119294	AC119294 Rattus no
25	40.4	3.1	195549	2	AC012019	AC012019 Homo sapi
26	40	3.1	12204	1	AE005112	AE005112 Halobacte
27	40	3.1	22407	1	RSO24581	AE005112 Halobacte
28	40	3.1	30350	1	YSC93315	AJ745811 Ralstonia
29	40	3.1	194334	2	AC101527	U10398 Saccharomyc
30	40	3.1	197050	1	AL646081	AC101527 Mus muscu
31	40	3.1	341887	1	AP003006	AL646081 Ralstonia
32	39.8	3.0	156683	2	AC118778	AP003006 Mesophizo
33	39.6	3.0	10293	1	AE005012	AC118778 Rattus no
34	39.6	3.0	73476	2	AC101502	AE005012 Halobacte
35	39.6	3.0	234817	10	AL663048	AC101502 Mus muscu
36	39.4	3.0	71517	8	AC073862	AL663048 Mouse DNA
37	39.4	3.0	125020	9	AF429315	AC073862 Homo sapi
38	39.2	3.0	91609	8	AC090206	AF429315 Homo sapi
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43	39	3.0	248362	2	AC125460	AC092779 Oryza sat
44	38.8	3.0	325	5	HSTNT5A	AC125460 Mus muscu
45	38.8	3.0	489	9	HSTNT5B	X79855 H.sapiens H
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ALIGNMENTS

RESULT 1				
AR093367				
LOCUS	AR093367	1305 bp	DNA	linear
DEFINITION	Sequence 19 from patent US 6001369.			
ACCESSION	AR093367			
VERSION	AR093367.1	GI:10020117		
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
	Unclassified.			
REFERENCE	1 (bases 1 to 1305)			
AUTHORS	Cochran,M.D. and Junker,D.E.			
TITLE	Recombinant fowlpox viruses and uses thereof			
JOURNAL	Patent: US 6001369-A 19 14-Dec-1999;			
FEATURES	Location/Qualifiers			


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RESULT 3
ILU28832 18912 bp DNA 1linear VRL 09-AUG-1996
DEFINITION Infectious laryngotracheitis virus US10, US2, protein kinase, U147,
glycoprotein G, ORF5, glycoprotein D, glycoprotein I, glycoprotein
E, ORF9 genes, complete cds.
ACCESSION U28832
VERSION U28832.1 GI:1486484

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KEYWORDS Infectious laryngotracheitis virus.
SOURCE Gallid herpesvirus 1
ORGANISM Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.
REFERENCE 1 (bases 1 to 18912)
AUTHORS Wild,M.A., Cook,S. and Cochran,M.
TITLE A genomic map of Infectious laryngotracheitis virus and the
sequence and organization of genes present in the unique short and
flanking regions
JOURNAL Virus Genes 12 (2), 107-116 (1996)
MEDLINE 9703380
PUBMED 8879127
REFERENCE 2 (bases 1 to 18912)
AUTHORS Wild,M.A.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-1995) Martha A. Wild, Syntro Research Laboratory,
3535 General Atomics Court, San Diego, CA 92121, USA
FEATURES
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RESULT 4
LOCUS HSMGDGLYCO 1627 bp DNA 1linear VRL 06-MAY-1996
DEFINITION Gallid herpesvirus 1 glycoprotein D (9D) gene, complete cds.

ACCESSION U31965
VERSION U31965.1 GI:493595
KEYWORDS glycoprotein D.
SOURCE Gallid herpesvirus 1.
ORGANISM Gallid herpesvirus 1
VIRUSES: dsDNA viruses, no RNA stage: Herpesviridae:
Alphaherpesvirinae: Infectious laryngotracheitis-like viruses.
1 (bases 1 to 1627)
AUTHORS Johnson, M.A., Tyack, S.G., Prideaux, C.T., Kongsuwan, K. and Sheppard, M.
TITLE Sequence characteristics of a gene in infectious laryngotracheitis virus homologous to glycoprotein D of herpes simplex virus
JOURNAL DNA Seq. 5 (3), 191-194 (1995)
MEDLINE 9537426
PUBMED 7612933
FEATURES
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1507..1517
polya_signal
BASE COUNT 410 a 428 c 428 g 361 t
ORIGIN
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Best Local Similarity 98.94; Pred. No. 0;
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Db 515 GTCCAGCTCAACCCGATTTCATACGTGGACACATGATATGCGGGCCAAAGAAAGAG 574
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RESULT 5
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LOCUS A22122 3502 bp DNA linear PAT 22-JUN-1994
DEFINITION ILTV gp60 gene.
ACCESSION A22122
VERSION A22122.1 GI:583833
KEYWORDS
SOURCE Gallid herpesvirus 1.
ORGANISM Gallid herpesvirus 1

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• FEATURES

source

location/Qualifiers

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Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.

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BASE COUNT 845 a 969 c 920 g 768 t

ORIGIN

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Best Local Similarity 98.6%; Pred. No. 3.2e-85;
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Db 3494 GTGAGCTC 3502

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RESULT 6
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LOCUS AF081810 161046 bp DNA circular VRL 08-MAR-1999
DEFINITION Lymantria dispar nucleopolyhedrovirus, complete genome.
ACCESSION AF081810
VERSION AF081810.1 GI:3822234

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KEYWORDS	LYMANTIRIA DISPAR NUCLEOPOLYHEDROVIRUS.
SOURCE	LYMANTIRIA DISPAR NUCLEOPOLYHEDROVIRUS
ORGANISM	Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
REFERENCE	1 (bases 1 to 161046)
AUTHORS	Kuzio,J., Pearson,M.N., Harwood,S.H., Funk,C.J., Evans,J.T., Slavicek,J.M. and Rohmann,G.F.
TITLE	Sequence and analysis of the genome of a baculovirus pathogenic for Lymantiria dispar
JOURNAL	Virology 253 (1), 17-34 (1999)
MEDLINE	99124785
PubMed	9687315
REFERENCE	2 (bases 1 to 161046)
AUTHORS	Kuzio,J., Pearson,M.N., Harwood,S.H., Funk,C.J., Evans,J.T., Slavicek,J. and Rohmann,G.F.
TITLE	Direct Submission
JOURNAL	Submitted (03-AUG-1998) Department of Microbiology, Oregon State University, Corvallis, OR 97331-3804, USA
REFERENCE	3 (bases 1 to 161046)
AUTHORS	Kuzio,J.
TITLE	Direct Submission
JOURNAL	Submitted (08-MAR-1999) NCBI, 8600 Rockville Pike, Bethesda, MD 20894, USA
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RESULT 7
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 DEFINITION M.xanthus sigma factor (rpoD) gene, complete cds.
 ACCESSION M32347
 VERSION M32347.1 GI:150117
 KEYWORDS sigma factor.
 SOURCE M.xanthus (strain FB (DZF1) DNA, clones psiG0[1,2].
 ORGANISM Myxococcus xanthus
 Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
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 1 (bases 1 to 2676)
 REFERENCES
 1 Inouye S.
 Cloning and DNA sequence of the gene coding for the major sigma
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 J. Bacteriol. 172 (1), 80-85 (1990)
 JOURNAL PUBMED 90094274
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SOURCE Myxococcus xanthus.
ORGANISM Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
Myxococcales; Cytophacterales; Myxococcaceae; Myxococcus.
REFERENCE 1 (bases 4593 to 7280)
AUTHORS Inouye, S.
TITLE Cloning and DNA sequence of the gene coding for the major sigma
factor from Myxococcus xanthus
JOURNAL J. Bacteriol. 172 (1), 80-85 (1990)
MEDLINE 90094274
PUBMED 2104614
REFERENCE 2 (bases 1 to 7980)
AUTHORS Davis, J.M., Mayor, U. and Plamann, L.
TITLE A missense mutation in rpoD results in an A-signalling defect in
Myxococcus xanthus
JOURNAL Mol. Microbiol. 18 (5), 943-952 (1995)
MEDLINE 96422481
PUBMED 8825098
REFERENCE 3 (bases 1 to 7980)
AUTHORS Plamann, L.S.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1995) Lynda S Plamann, Department of Biology,
Texas A & M University, College Station, TX 77843-3258, USA
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DEFINITION	Mus musculus clone RP24-178p12, WORKING DRAFT SEQUENCE, 16 ordered pieces.				
ACCESSION	AC121079				
VERSION	AC121079.3	GI:22381013			
KEYWORDS	HTG; HFGS_PHASE2; HFGS_DRAFT; HFGS_FULLTOP.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 185663)				
AUTHORS	Bitren,B., Nusbaum,C. and Lander,E.				
TITLE	Mus musculus chromosome, clone RP24-178p12				
JOURNAL	unpublished				
REFERENCE	2 (bases 1 to 185663)				
AUTHORS	Bitren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,				

Anderson, S., Barina, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhvalter, B., Brown, A., Camarata, J., Campiolano, A., Chang, J.,
Chazaro, B., Choepl, Y., Colangelo, M., Collins, S., Collimore, J.,
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Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
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Hagos, B., Horton, L., Hulme, M., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, K., Kells, C., Lacroque, K., Lamasaras, R.,
Landers, T., Lehoczyk, J., Levine, R., Lindblad-ton, K., Liu, G.,
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Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
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Seman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Triggilo, J., Vassiliou, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.-J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE	JOURNAL	REFERENCE	AUTHORS
Direct Submission		Submitted (15-Nov-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	
		3 (bases 1 to 185863)	
			Bliren,B., Nussbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boulhache,A., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fero,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardys,A., Gord,S., Graham,L., Grand-pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Linblad-Poh,K., Liu,G., Maclean,C., MacDonald,P., Major,J., Matthews,C., McCatchy,M., Meldrim,J., Menues,L., Milnova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Plunhbang,P., Pierre,N., Raymond,C., Retta,R., Risse,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schnupack,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Vael,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zalnoun,J., Zemek,L., Zimmer,A. and Zody,M.
Direct Submission		Submitted (21-Aug-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	
		On Aug 21, 2002 this sequence version replaced gi:20806332.	
		All repeats were identified using repeatmasker:	
		Smith, A.F.A. & Green, P. (1996-1997)	
		http://ftp.genome.washington.edu/rm/Repeatmasker.html	

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIMR
 Web site: <http://www.seq.wi.mit.edu>
 Contact: sequence.submissions@genome.wi.mit.edu
 -----Project Information


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DEFINITION  Neurospora crassa DNA linkage group V BAC contig BLN2.  
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VERSION     AL513444.1 GI:12718373  
KEYWORDS    .  
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REFERENCE   1  
AUTHORS     Schulte,U., Algn,V., Hohnesel,J., Brandt,P., Partmann,B.,  
Holland,R., Nyakatura,G., Wewes,H.W. and Mannhaupt,G.  
TITLE       Unpublished  
JOURNAL     German Neurospora genome/project.  
AUTHORS     Submitted (08-NOV-2001) MIPS, Institut fuer Bioinformatik,  
           GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH,  
           Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail:  
           G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute  
           of Biotechnology, Heinrich-Heine-University, D-40225 Duesseldorf,  
           E-mail: ulrich.schulte@uni-duesseldorf.de  
COMMENT     Sequencing was performed by MWG Biotech AG, Ebersberg, Germany,  
           http://www.mwgdna.com  
           This contig is an assembly of BAC BLN2 from 1 to: 91660, strain  
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           PLORI5TR6xh, strain 74-OR-23-1A; BAC and cosmid clones are available  
           at the fungal Genetic Stock Center, http://www.fgsc.net  
           Information on performance of analysis and a more detailed  
           annotation of this entry and other sequences of linkage groups II  
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Location/Qualifiers
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gene

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence

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Search completed: February 25, 2003, 14:53:27
Job time : 4114 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 25, 2003, 12:00:13 ; Search time 308 Seconds

(without alignments)
9541.746 Million cell updates/sec

Title: US-09-994-064-10

Perfect score: 1305
Sequence: 1 ATGCACCGCTCTATCTCAG.....TAAATGCGCGCTACTATA 1305

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1305	100.0	1305	15	gd gene of infecti
2	1305	100.0	1305	16	infectious laryngo
3	1305	100.0	1305	20	Seq ID No: 19 of U
4	1305	100.0	1305	21	Recombinant fowlp
5	1305	100.0	1305	21	ILTV glycoprotein
6	1305	100.0	13473	16	Infectious laryngo
7	1305	100.0	13473	17	Infectious laryngo
8	1305	100.0	18912	17	Infectious laryngo
9	361	27.7	3502	13	Sequence of ILTV g

	10	42	3.2	42	17	AA044399
	11	41.6	3.2	390	13	AA021833
	12	41.6	3.2	390	12	AA036859
	13	41.6	3.2	390	22	AA076910
	14	41.6	3.2	390	24	AA072775
	15	38.4	2.9	1761	21	AA04461
	16	38.2	2.9	1232	23	AB011609
	17	38.2	2.9	3038	23	AB016776
	18	38.2	2.9	3232	23	AB011608
	19	37.4	2.9	2277	19	AA013834
	20	37.4	2.9	2277	19	AA013834
	21	36.8	2.8	720	24	AB033458
	22	36.8	2.8	1450	12	AA013227
	23	36.8	2.8	1450	12	AA013408
	24	36.8	2.8	3325	23	AB022263
	25	36.8	2.8	3325	23	AB028100
	26	36.8	2.8	3325	23	AB029043
	27	36.8	2.8	3395	21	AA000601
	28	36.8	2.8	5895	23	AB087076
	29	36.8	2.8	2943	17	AA016480
	30	36.2	2.7	429	20	AA027978
	31	35.6	2.7	429	21	AA096005
	32	35.6	2.7	429	21	AA096005
	33	35.6	2.7	1680	23	AA068558
	34	35.6	2.7	2428	22	AA029596
	35	35.6	2.7	3642	21	AA096040
	36	35.6	2.7	4091	21	AA096039
	37	35.6	2.7	4422	21	AA028685
	38	35.6	2.7	5610	20	AA028008
	39	35.6	2.7	5610	21	AA096035
	40	35.6	2.7	5610	21	AA096041
	41	35.6	2.7	5659	21	AA087686
	42	35.6	2.7	1364	14	AA035092
	43	35.4	2.7	3489	21	AA030290
	44	35.4	2.7	3489	22	AA082901
	45	35.4	2.7	3489	22	AA082901

ALIGNMENTS

RESULT 1
ID AA068944 standard; DNA: 1305 BP.
AC AA068944;
XX
XX
DT 13-APR-1995 (first entry)
XX
DE gd gene of infectious laryngotracheitis virus (ILT).
XX
KW Homology vector 586-36.6; gd gene; cassette gene; ss.
XX
OS Infectious laryngotracheitis virus.
XX
FH Key location/Qualifiers
FT CDS 1..1305
FT /*tag= a
XX
XX MO9419014-A.
XX
XX PD 01-SEP-1994.
XX
XX PF 28-FEB-1994; 94WO-US01826.
XX
XX PR 26-FEB-1993; 93US-0024156.
XX
XX PA (JAPG) NIPPON ZEON KK.
XX (SYTR) SYNTRON CORP.
XX
XX PI Cochran MD;
XX
XX DR WPI; 1994-294007/36.

DR P-PSDB: AAR58856.
 XX New recombinant fowl pox virus for use in vaccines - contains
 PT genes expressing antigens of Newcastle disease virus and opt.
 PT Infectious bronchitis virus
 XX
 PS Disclosure: Page 74-75; 85pp; English.
 XX
 CC AA068944 contains the coding region of the ILT gd gene and was
 CC derived from an approx. 2060 bp EcoRI to BclI restriction sub-
 CC fragment of the ILT KpnI genomic restriction fragment #8 (10.6kb).
 CC It is part of a cassette in plasmid 586-36.6 constructed for
 CC the purpose of inserting ILT gb and gd genes into the fowlpox
 CC virus (FPV).
 XX
 SQ Sequence 1305 BP; 331 A; 349 C; 344 G; 281 T; 0 other;

Query Match 100.0%; Score 1305; DB 15; Length 1305;
 Best Local Similarity 100.0%; P-Id. No. 0;
 Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCACGCTCCTCATCTCAGACGACACTGCGTTACTACGCGGAAGAGAGAGGCTTAAAC 60
 DB 1 ATGCACGCTCCTCATCTCAGACGACACTGCGTTACTACGCGGAAGAGAGGCTTAAAC 60
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 DB 61 AAACACATGATTCGCGTGAAGAAACGGTGTCTCAGGCGCAGCTGATTCACCTTTTC 120
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 DB 121 TGGACTGTGTCCAGATTATGCGGGAGCATATCTGCTTTGACCAACGCTATGACCGC 180
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 QY 241 AGCAGCGCGCGCGTACGACTACATTTTAGCGCGTGCAGCGGCTAAC 300
 DB 241 AGCAGCGCGCGCGTACGACTACATTTTAGCGCGTGCAGCGGCTAAC 300
 QY 301 ATACCGCGGTTGGCCGCTTAACAGATCTCACTAGGATACAGAGCTGCGAGCTT 360
 DB 301 ATACCGCGGTTGGCCGCTTAACAGATCTCACTAGGATACAGAGCTGCGAGCTT 360
 QY 361 GTGAGCTCAACCGATTTCTAACGTGAGACATGATATGCGCGCAAGAAAGAG 420
 DB 361 GTGAGCTCAACCGATTTCTAACGTGAGACATGATATGCGCGCAAGAAAGAG 420
 QY 421 AAGGGGGCCCTTTCGAGGCTCCGTCGTGTTTACCTGATTAAGGCGCAGCAGCGC 480
 DB 421 AAGGGGGCCCTTTCGAGGCTCCGTCGTGTTTACCTGATTAAGGCGCAGCAGCGC 480
 QY 481 GAGGACAGTACTGTCCAATCTATAGAAAAGATACAGGGAATGTGGCGAGTACAG 540
 DB 481 GAGGACAGTACTGTCCAATCTATAGAAAAGATACAGGGAATGTGGCGAGTACAG 540
 QY 541 CTATCTGATTCGCGCTTCAATCTGACAGATGTGGCAGTGTATGTTCTTACAC 600
 DB 541 CTATCTGATTCGCGCTTCAATCTGACAGATGTGGCAGTGTATGTTCTTACAC 600
 QY 601 CTGTGATTCGCGAAATGGCGGAGTACATATCTCCCACTGCTGCTTCTG 660
 DB 601 CTGTGATTCGCGAAATGGCGGAGTACATATCTCCCACTGCTGCTTCTG 660
 QY 661 CAATACCTGCTGACCTGAAAATCGGAGATTTCGCAAAACAGCTCTCTACTAGAA 720
 DB 661 CAATACCTGCTGACCTGAAAATCGGAGATTTCGCAAAACAGCTCTCTACTAGAA 720
 QY 721 GTTAACGATCGCTGTTTAAAGATCGGTCGACGTTAACTTTTACCGGAAATGCTGG 780
 DB 721 GTTAACGATCGCTGTTTAAAGATCGGTCGACGTTAACTTTTACCGGAAATGCTGG 780

QY 781 AACACAGACAGTATGACACTGATTTCAAGCCAGACACTTTTATCCGATCGCAGAC 840
 DB 781 AACACAGACAGTATGACACTGATTTCAAGCCAGACACTTTTATCCGATCGCAGAC 840
 QY 841 AATACAGACAGCGGAGCAGAGTATTCGGGATACGAAATATTTGCGAGCGGTGGAT 900
 DB 841 AATACAGACAGCGGAGCAGAGTATTCGGGATACGAAATATTTGCGAGCGGTGGAT 900
 QY 901 AATTGCTGAGAAAAGAAATCTAGCGCGCAGACCTGCTGCAGATAGCCTCCGCA 960
 DB 901 AATTGCTGAGAAAAGAAATCTAGCGCGCAGACCTGCTGCAGATAGCCTCCGCA 960
 QY 961 GAATTCGCGCTGTAACCAAGAAAGCGAAGGCGCACCCCGGACGAGCAAGACAGCAA 1020
 DB 961 GAATTCGCGCTGTAACCAAGAAAGCGAAGGCGCACCCCGGACGAGCAAGACAGCAA 1020
 QY 1021 AAGAAAGCCCTCCAGAGACTCGAGAGACATGACATGACAGGCTTGTGAGAAAT 1080
 DB 1021 AAGAAAGCCCTCCAGAGACTCGAGAGACATGACATGACAGGCTTGTGAGAAAT 1080
 QY 1081 CTGCGCGCTTCCCGAAGACAGAAAGTCCCGAGACACCGAGACAGATATCCAAAC 1140
 DB 1081 CTGCGCGCTTCCCGAAGACAGAAAGTCCCGAGACACCGAGACAGATATCCAAAC 1140
 QY 1141 TCGGATCTGACTATTTCAATGACATGACATGACATGACATGACATGACATGACAT 1200
 DB 1141 TCGGATCTGACTATTTCAATGACATGACATGACATGACATGACATGACATGACAT 1200
 QY 1201 AGTTTAATGCGCTTCATGCCATATTCGCGCGTGTGATGCTGCGCGGCTG 1260
 DB 1201 AGTTTAATGCGCTTCATGCCATATTCGCGCGTGTGATGCTGCGCGGCTG 1260
 QY 1261 GTGGGGCTACTGTTTGGAGCATGTAATAATGCGCGTACTAA 1305
 DB 1261 GTGGGGCTACTGTTTGGAGCATGTAATAATGCGCGTACTAA 1305

RESULT 2
 AAT33505
 ID AAT33505 standard; DNA; 1305 BP.
 XX
 AC AAT33505;
 XX
 DT 19-NOV-1996 (first entry)
 XX
 DE Infectious laryngotracheitis virus gd gene.
 XX
 KW Infectious laryngotracheitis virus; ILTV; herpesvirus;
 KW attenuation; vector; vaccine; chicken; poultry; immunisation;
 KW glycoprotein gp; ds.
 XX
 OS Infectious laryngotracheitis virus.
 XX
 PN W09508622-AL.
 PN
 PD 30-MAR-1995.
 PD
 XX
 PF 16-SEP-1994; 94WO-US10628.
 PF
 PR 24-SEP-1993; 93US-0126597.
 PR
 XX
 PA (SYTR) SYNTRO CORP.
 PA
 PI Cochran MD, Wild MA;
 PI
 XX
 DR WPI: 1995-139591/18.
 DR
 P-PSDB: AAM00638.
 XX
 PT Recombinant attenuated infectious laryngotracheitis virus - for use
 PT in vaccines to protect poultry from infection from the virus, also
 PT methods of distinguishing between vaccinated and naturally infected
 PT birds

PS Example 1; Page 106-107; 177bp; English.

CC The gp gene (AAT33505) spans bases 8462-9766 of the unique short
 CC region (see also AAT33504) of infectious laryngotracheitis virus
 CC (ILTV) genomic DNA. It codes for a glycoprotein (AAM00638) of
 CC approx. 48,477 mol.wt. that is homologous to pseudorabies
 CC virus gD and to gp from herpes simplex virus-1. Marek's
 CC disease virus, IPV and bovine herpesvirus-1.1. Monoclonal
 CC antibodies raised to ILTV react specifically with gp from
 CC ILTV and also with ILTV gp expressed in herpesvirus of
 CC turkeys (HVT) virus vector. ILTV gp expressed in the HVT
 CC vector is useful as a subunit vaccine.

XX Sequence 1305 BP; 331 A; 349 C; 344 G; 281 T; 0 other;

Query Match: 100.0%; Score 1305; DB 16; Length 1305;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCACGTCGTCATCTCAGACGCGACCTGCGTTACTACGCGAAGAGAGTGTCTTAC 60
 DB 1 ATGCACGTCGTCATCTCAGACGCGACCTGCGTTACTACGCGAAGAGAGTGTCTTAC 60
 QY AACACATGATGATGCGGTGGAAGAAAGGTGCTGCTCAGAGCGCAGCTGATTCACTTTTC 120
 DB AACACATGATGATGCGGTGGAAGAAAGGTGCTGCTCAGAGCGCAGCTGATTCACTTTTC 120
 QY 121 TGGACTGTGTGTCAGATTATGCGGAGACATATCTGCTTTGTAGCAACGCTATGACCGC 180
 DB 121 TGGACTGTGTGTCAGATTATGCGGAGACATATCTGCTTTGTAGCAACGCTATGACCGC 180
 QY 181 CATTATTTTGGAGAAATGTTTTGACTATGTAAGTGTCTTCTCTCTCGCTAGCAG 240
 DB 181 CATTATTTTGGAGAAATGTTTTGACTATGTAAGTGTCTTCTCTCTCGCTAGCAG 240
 QY 241 AGCAGCGCGCGCTCAGTACGACATATTTAGGCCGCTGCGCGCTCAGCGCTAAC 300
 DB 241 AGCAGCGCGCGCTCAGTACGACATATTTAGGCCGCTGCGCGCTCAGCGCTAAC 300
 QY 301 ATACCGGCGGTGGCCGCTATTAACAGATCTCACTAGGGTATCAAGAGGCTCGACGTT 360
 DB 301 ATACCGGCGGTGGCCGCTATTAACAGATCTCACTAGGGTATCAAGAGGCTCGACGTT 360
 QY 361 GTGAGCTCAACCCGATTTCTAACGTGAGACATGATATGCGCGCAAGAAAGAG 420
 DB 361 GTGAGCTCAACCCGATTTCTAACGTGAGACATGATATGCGCGCAAGAAAGAG 420
 QY 421 AAGGGGGGCCCTTTCGAGGCTCCGTCGTCTGTTCTACGTTAAGGCGCAGCAGCGC 480
 DB 421 AAGGGGGGCCCTTTCGAGGCTCCGTCGTCTGTTCTACGTTAAGGCGCAGCAGCGC 480
 QY 481 GAGGACAGTACTGTCCAAATCTATAGAAAAGATACAGGGAATGTGGCGACGTACAACTG 540
 DB 481 GAGGACAGTACTGTCCAAATCTATAGAAAAGATACAGGGAATGTGGCGACGTACAACTG 540
 QY 541 CTATCTGAATGGCGCGTCAATCTGACAGATGTGGGCAATGATATGTTCTCTAGACC 600
 DB 541 CTATCTGAATGGCGCGTCAATCTGACAGATGTGGGCAATGATATGTTCTCTAGACC 600
 QY 601 CTGTGATCGGAAATGGCGGAGCTGACTATATTTCTCCCGCAGCTGCGCTCTGGC 660
 DB 601 CTGTGATCGGAAATGGCGGAGCTGACTATATTTCTCCCGCAGCTGCGCTCTGGC 660
 QY 661 CAATACTTGCTGACCTGAAAATCGGAGATTGCGCAAAACAGCTCTCGTAACCTAGAA 720
 DB 661 CAATACTTGCTGACCTGAAAATCGGAGATTGCGCAAAACAGCTCTCGTAACCTAGAA 720
 QY 721 GTTAAGGATCGCTGTTTAAAGATCGGCTGACACTTATCTTTACCCTGGAATGCTGG 780
 DB 721 GTTAAGGATCGCTGTTTAAAGATCGGCTGACACTTATCTTTACCCTGGAATGCTGG 780
 QY 781 ACAAGACAGATGATCAGACTGGATTCAAGGGAAACACCTTATCCGATCGCAGACAC 840
 DB 781 ACAAGACAGATGATCAGACTGGATTCAAGGGAAACACCTTATCCGATCGCAGACAC 840

DB 781 ACAAGACAGATGATCAGACTGGATTCAAGGGAAACACCTTATCCGATCGCAGACAC 840
 QY 841 AATACAGACACGCGGAGCAGCATATATCGGGATACGAAATATTTGACGCGCTGGAAT 900
 DB 841 AATACAGACACGCGGAGCAGCATATATCGGGATACGAAATATTTGACGCGCTGGAAT 900
 QY 901 AATTGTGTAGGAAAAAAGAAATCTCAGAGCGCCAGACCTCTGTCAGATACGTCGCCAA 960
 DB 901 AATTGTGTAGGAAAAAAGAAATCTCAGAGCGCCAGACCTCTGTCAGATACGTCGCCAA 960
 QY 961 GAAATTCCTCTGTAAACCAAGAAAGCGGAGCGCACCCCGAGCAGAGAGCGAA 1020
 DB 961 GAAATTCCTCTGTAAACCAAGAAAGCGGAGCGCACCCCGAGCAGAGAGCGAA 1020
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 DB 1021 AAGAAGGCCCTTCAGAAAGCTCGGAGAGCAGATGACGAGCGTCTTGAGAAAAT 1080
 QY 1081 CTTGCGCGCCCTCCCGGAGAGCAGAAAGTCCCGAGAGACACCGACGATGATCCAAAC 1140
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 QY 1141 TCGGATCTGACTATATTAATGACATGCCCGCTGATCCCGGTGAGAGACTACTAAA 1200
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 DB 1201 AGTTCTAATGCCGTCTCCATGCCCATTATGCGCGGCTTCGTAGCTGCGGCTGCTC 1260
 QY 1261 GTGGGGCTACTGTTGTGGAGATCGTAAATGGCGGCTAGACTAA 1305
 DB 1261 GTGGGGCTACTGTTGTGGAGATCGTAAATGGCGGCTAGACTAA 1305

RESULT 3

AA81152
 ID AA81152 standard; DNA; 1305 BP.

AC AA81152;

DT 07-SEP-1999 (first entry)

DE Seq ID No: 19 of US5925358.

XX Fowlpox virus; FPV; recombinant; vaccine; immunisation; chicken; NDV;
 KW Newcastle disease virus; NDV; Fowlpox; Infectious laryngotracheitis; ds-
 OS Fowlpox virus.

PN US5925358-A.

XX 20-JUL-1999.

PD 07-JUN-1995; 95US-0484575.

PF 07-JUN-1995; 95US-0484575.

PR 26-FEB-1993; 93US-0024156.

PR 28-FEB-1994; 94WO-US02252.

XX (SYTR) SYNPRO CORP.

XX Cochran MD, Junker DE;

XX WPI; 1999-418249/35.

DR P-PSDB; AAY21984.

PT Fowlpox viruses, useful as vaccines for immunization of
 PT chickens/turkeys against Fowlpox and Newcastle disease.virus

PS Disclosure; Columns 77-82; 108bp; English.

XX The invention relates to a recombinant fowlpox virus (FPV) comprising

CC a foreign DNA inserted into a region of the fowlpox virus genome
 CC corresponding to a 2.8 kb EcoRI fragment, capable of being expressed in a
 CC host cell. The virus is used as a vaccine for immunising chickens against
 CC Newcastle disease virus (NDV), Fowlpox, and infectious laryngotracheitis.
 XX

Sequence 1305 BP; 331 A; 349 C; 344 G; 281 T; 0 other;

Query Match 100.0%; Score 1305; DB 20; Length 1305;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGACCCGCTCTATCTCAAGCGGACCTCGCTTACTACGGAAAGAGAGGTGCTTAC 60
DB 1 ATGACCCGCTCTATCTCAAGCGGACCTCGCTTACTACGGAAAGAGAGGTGCTTAC 60
QY 61 AACACATGATGCGGTGGAACAGGTGCTGTCAGGCGCCAGCTGATTCATCTTTTC 120
DB 61 AACACATGATGCGGTGGAACAGGTGCTGTCAGGCGCCAGCTGATTCATCTTTTC 120
QY 121 TGACCTTGTGTCAGATTATGCGGAGCATATCTGCTTGTACGAACGCTATGACCGC 180
DB 121 TGACCTTGTGTCAGATTATGCGGAGCATATCTGCTTGTACGAACGCTATGACCGC 180
QY 181 CATTTATTTTGAAGATGCTTTTGGACTATGCTACTGCTTCTCTGCTAGCCAG 240
DB 181 CATTTATTTTGAAGATGCTTTTGGACTATGCTACTGCTTCTCTGCTAGCCAG 240
QY 241 AGCAGCGCGCCGCTCAGCTACGACTATTTAGCGCGCGCTGCGCGCTAAC 300
DB 241 AGCAGCGCGCGCTCAGCTACGACTATTTAGCGCGCGCTGCGCGCTAAC 300
QY 301 ATACCGCGGCTTGCCCGCTATTAACAGATACCTCCTAGGGTATCAAGAGCTGCGAGTT 360
DB 301 ATACCGCGGCTTGCCCGCTATTAACAGATACCTCCTAGGGTATCAAGAGCTGCGAGTT 360
QY 361 GTGAGCTCAACCCGATTTCTAACGTCGACGATATTCGGCGCCAAAGAAAAAG 420
DB 361 GTGAGCTCAACCCGATTTCTAACGTCGACGATATTCGGCGCCAAAGAAAAAG 420
QY 421 AAGGGGGGCGCTTTCAGGCGCTCCGCTGCTGCTTCTACGTTTAAAGGCGCAGCGC 480
DB 421 AAGGGGGGCGCTTTCAGGCGCTCCGCTGCTGCTTCTACGTTTAAAGGCGCAGCGC 480
QY 481 GAGGACAACTACTGTCATCTATAGAAAAGATACAGGAAATGCGCAGCTACACTG 540
DB 481 GAGGACAACTACTGTCATCTATAGAAAAGATACAGGAAATGCGCAGCTACACTG 540
QY 541 CTATCTGAATGCGCGCTTCAATCTGCACAGATGTGGGAGTGAGCATGTGCTAGCACC 600
DB 541 CTATCTGAATGCGCGCTTCAATCTGCACAGATGTGGGAGTGAGCATGTGCTAGCACC 600
QY 601 CTTGATGCGGAAATGCGCGGAGCTGACTATATTTCTCCCACTGCTGCTCTGCG 660
DB 601 CTTGATGCGGAAATGCGCGGAGCTGACTATATTTCTCCCACTGCTGCTCTGCG 660
QY 661 CAATCTGCTGACCTGTAATTCGGAATGTTGGCAAAACAGCTCTGTAACCTAGAA 720
DB 661 CAATCTGCTGACCTGTAATTCGGAATGTTGGCAAAACAGCTCTGTAACCTAGAA 720
QY 721 GTTAACGATCGCTGTTTAAAGATCGGTCGACGTTAACTTTTACCGTCGAATGTGG 780
DB 721 GTTAACGATCGCTGTTTAAAGATCGGTCGACGTTAACTTTTACCGTCGAATGTGG 780
QY 781 ACAACAGAACTATCAACACTGATTTCAAGCGCAACCTTTATCCATGCAACAC 840
DB 781 ACAACAGAACTATCAACACTGATTTCAAGCGCAACCTTTATCCATGCAACAC 840
QY 841 AATACACAGACGCGGAGAGCTATATGGGGATACGAAGATTTCTGACGCTGGAAT 900
DB 841 AATACACAGACGCGGAGAGCTATATGGGGATACGAAGATTTCTGACGCTGGAAT 900
QY 901 AATTGTGAGAAAAAATCTAGCGCGCAGACCTCTGCCAGATAGGTCGCCGAA 960
DB 901 AATTGTGAGAAAAAATCTAGCGCGCAGACCTCTGCCAGATAGGTCGCCGAA 960

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DB 901 AATTGTGAGAAAAAATCTAGCGCGCAGACCTCTGTCCAGATAGCTCCGCA 960
QY 961 GAAATTCGCGCTGTAAACCAAGAAAGCGGAAGGCGCACCCGAGCAGAAAGCAGCA 1020
DB 961 GAAATTCGCGCTGTAAACCAAGAAAGCGGAAGGCGCACCCGAGCAGAAAGCAGCA 1020
QY 1021 AAGAAGGCCCTCCAGAAAGCTCGGAGCAGCAATGACAGCAGAGCTTCTGAGAAAAAT 1080
DB 1021 AAGAAGGCCCTCCAGAAAGCTCGGAGCAGCAATGACAGCAGAGCTTCTGAGAAAAAT 1080
QY 1081 CCGCGCCCTCCCGAGAGCAGAGAGTCCCGAGAGACAGGAGCAGATGATCCAAAC 1140
DB 1081 CCGCGCCCTCCCGAGAGCAGAGAGTCCCGAGAGACAGGAGCAGATGATCCAAAC 1140
QY 1141 TCGGATCTGACTATTATCAATGACATGCCCCCGCTGATCCCGGTGAGAGACTATAA 1200
DB 1141 TCGGATCTGACTATTATCAATGACATGCCCCCGCTGATCCCGGTGAGAGACTATAA 1200
QY 1201 AGTTTAAATGCGCTCCATGCGCCATATTCGGGGGCTGTGATGCTCGCGGCTG 1260
DB 1201 AGTTTAAATGCGCTCCATGCGCCATATTCGGGGGCTGTGATGCTCGCGGCTG 1260
QY 1261 GTGGGGCTACTGTTTGAAGCATCTTAAATGCGCGCTAGCTAA 1305
DB 1261 GTGGGGCTACTGTTTGAAGCATCTTAAATGCGCGCTAGCTAA 1305

```

RESULT 4
 AAC67867
 ID AAC67867 standard; DNA; 1305 BP.

XX AAC67867;

XX 02-MAR-2001 (first entry)

XX Recombinant fowlpox virus-related polynucleotide, SEQ ID NO: 19.

XX Fowlpox virus; FPV; antiviral; antibacterial; vaccine;

XX Newcastle's disease; Marek's disease; infectious laryngotracheitis; ds.

XX Unidentified.

XX US6136318-A.

XX 24-OCT-2000.

XX 07-JUN-1995; 95US-0486414.

XX 26-FEB-1993; 93US-0024156.

XX 28-FEB-1994; 94WO-US02252.

XX (JUNK/) JUNKER D E.

XX (COCH/) COCHRAN M D.

XX Cochran MD, Junker DE;

XX WPI: 2000-686071/67.

XX New recombinant fowlpox virus useful as vaccines contains foreign DNA

XX inserted into specific non-essential region of the genome

XX Disclosure: Column 77-80; 56pp; English.

XX The present sequence is provided in a specification relating to a
 CC recombinant fowlpox virus (FPV) that comprises a foreign DNA inserted
 CC within a 3.5 kb EcoRI fragment of the FPV genomic DNA. The foreign DNA
 CC can be expressed in host cells infected with FPV. The recombinant FPV
 CC may be used in vaccines to protect animals (especially chickens) against
 CC fowlpox and, depending on the source of the foreign DNA, other diseases,
 CC particularly Newcastle's disease, Marek's disease or infectious
 CC laryngotracheitis.

XX Sequence 1305 BP; 331 A; 349 C; 344 G; 281 T; 0 other;

Query Match 100.0%; Score 1305; DB 21; Length 1305;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGACCGCTCTCATCTTCAGACGACACTCGGCTTACTACGCGAAAGAGAGAGTGTTCAC 60
DB 1 ATGACCGCTCTCATCTTCAGACGACACTCGGCTTACTACGCGAAAGAGAGAGTGTTCAC 60
QY 61 AAACACATGATGATGGGTGGAAGAAAGCGTGTCTCAGGCGCAGCTGATATCACTCTTTTC 120
DB 61 AAACACATGATGATGGGTGGAAGAAAGCGTGTCTCAGGCGCAGCTGATATCACTCTTTTC 120
QY 121 TGGAGCTGTCTCAGGATATTCGCGGAGCATATCTGCTTTGACGCAAGCATATGAGACCGC 180
DB 121 TGGAGCTGTCTCAGGATATTCGCGGAGCATATCTGCTTTGACGCAAGCATATGAGACCGC 180
QY 181 CATTTATTTTGGAGAAATGCTTTTGGACATCTGACTGCTTTCCTCTGCTAGCCAG 240
DB 181 CATTTATTTTGGAGAAATGCTTTTGGACATCTGACTGCTTTCCTCTGCTAGCCAG 240
QY 241 AGCACCGCGCGCTGACGATACGATATTTAGGCGCTGCGGCTCGACGCGCTAAC 300
DB 241 AGCACCGCGCGCTGACGATACGATATTTAGGCGCTGCGGCTCGACGCGCTAAC 300
QY 301 ATACCGGCGGCTTGGCCGCTATACAGATCTCTACAGGCTATCAAGAGGCTGGAGGTT 360
DB 301 ATACCGGCGGCTTGGCCGCTATACAGATCTCTACAGGCTATCAAGAGGCTGGAGGTT 360
QY 361 GTGAGGCTCAACCGGATTTTCAAGTGGAGACACATGATATGGGCGCCAAAGAAAGAG 420
DB 361 GTGAGGCTCAACCGGATTTTCAAGTGGAGACACATGATATGGGCGCCAAAGAAAGAG 420
QY 421 AAGGGGGGCTTTCGAGGCTCGCTGCTGTTTCAAGTATTAAGGGGAGGAGGAGCGC 480
DB 421 AAGGGGGGCTTTCGAGGCTCGCTGCTGTTTCAAGTATTAAGGGGAGGAGGAGCGC 480
QY 481 GAGGACAGTCTGTCACATCTATAGAAAGATACAGAGGAGATGGGAGGAGTACATG 540
DB 481 GAGGACAGTCTGTCACATCTATAGAAAGATACAGAGGAGATGGGAGGAGTACATG 540
QY 541 CTATCTGAATGCGCGCTTTCATCTGACAGATGAGGAGTGGAGCTATGTTCTTAGCACC 600
DB 541 CTATCTGAATGCGCGCTTTCATCTGACAGATGAGGAGTGGAGCTATGTTCTTAGCACC 600
QY 601 CTGTATTCGGAATGCGCGGAGCTGATATTTCTCCGACCTGCTGCGCTCTGCGC 660
DB 601 CTGTATTCGGAATGCGCGGAGCTGATATTTCTCCGACCTGCTGCGCTCTGCGC 660
QY 661 CAATACCTTGTGACCTGAAATCGGAGATTTGCGCAACAGCTCTGTAATCTAGAA 720
DB 661 CAATACCTTGTGACCTGAAATCGGAGATTTGCGCAACAGCTCTGTAATCTAGAA 720
QY 721 GTTACAGATGCTGTTTAAAGATGGGTCGAGTAACTTTTACGTCGAATGCGG 780
DB 721 GTTACAGATGCTGTTTAAAGATGGGTCGAGTAACTTTTACGTCGAATGCGG 780
QY 781 ACAACAGACAGTATCAGACTGATTTCAAGGCGACACCTTTATCCGATGCGACAGACC 840
DB 781 ACAACAGACAGTATCAGACTGATTTCAAGGCGACACCTTTATCCGATGCGACAGACC 840
QY 841 AATACAGACAGCGGAGCAGATATTCGCGGAGATACGAAGATATTTGACGCGCTGGAAT 900
DB 841 AATACAGACAGCGGAGCAGATATTCGCGGAGATACGAAGATATTTGACGCGCTGGAAT 900
QY 901 AATTGCGAGGAGAAAGAAATCTAGGCGCGCAGACCTGCTCAGATAGGCTCCCGAA 960
DB 901 AATTGCGAGGAGAAAGAAATCTAGGCGCGCAGACCTGCTCAGATAGGCTCCCGAA 960
QY 961 GAAATTCCTGCTTACCAAGAAAGCGAAGGCGCAGACCCGCGAGGAGAAAGCAGGAA 1020
DB 961 GAAATTCCTGCTTACCAAGAAAGCGAAGGCGCAGACCCGCGAGGAGAAAGCAGGAA 1020

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QY 1021 AAGAAGGCCCTCCAGAGACTCGGAGGAGACGACATGCGAGGAGGCTTCGAGAAAT 1080
DB 1021 AAGAAGGCCCTCCAGAGACTCGGAGGAGACGACATGCGAGGAGGCTTCGAGAAAT 1080
QY 1081 CCTGCCGCCCTCCCGAAGAGAGAGAGTCCCGAGACACCGACGACGATGATCCAAAC 1140
DB 1081 CCTGCCGCCCTCCCGAAGAGAGAGAGTCCCGAGACACCGAGACGAGATGATCCAAAC 1140
QY 1141 TCGATCTGACTATTTACATGACATGCGCCGCGTGTATCCCGGTGAGAGAGACTTAA 1200
DB 1141 TCGATCTGACTATTTACATGACATGCGCCGCGTGTATCCCGGTGAGAGACTTAA 1200
QY 1201 AGTTCTAATGCGGCTCCATGTCGAGATGCGGCGTTGTAAGCTGCGGCGGCTC 1260
DB 1201 AGTTCTAATGCGGCTCCATGTCGAGATGCGGCGGTTGTAAGCTGCGGCGGCTC 1260
QY 1261 GTGGGCTACTGTTTGGAGCATGTAAATGCCGCGCTAGCTAA 1305
DB 1261 GTGGGCTACTGTTTGGAGCATGTAAATGCCGCGCTAGCTAA 1305

RESULT 5
AA249300
ID AA249300 standard; cdna; 1305 BP.
XX
AC AA249300;
XX
DT 14-MAR-2000 (first entry)
XX
DE ILTV glycoprotein D (gp) gene.
XX
KW Fowlpox virus; FPV; recombinant; antigenic protein; expression;
KW Infectious laryngotracheitis virus; ILTV; Newcastle disease virus; NDV;
KW Marek's disease virus; cytokine; promoter; homologous recombination;
KW homology vector; multivalent; live vaccine; glycoprotein D; de.
XX
OS Infectious laryngotracheitis virus.
XX
FH Key
FT CDS 1..1305 Location/Qualifiers
FT FT /*tag= a
FT FT /product= "Glycoprotein D (gp)"
XX
PN US6001369-A.
XX
PD 14-DEC-1999.
XX
PE 07-JUN-1995; 95US-0477459.
XX
PR 26-FEB-1993; 93US-0024156.
PR 28-FEB-1994; 94WO-US02252.
XX
PA (SVTR ) SYNTRO CORP.
XX
PI Junker DE, Cochran MD;
XX
DR WPI: 2000-071638/06.
XX
DR P-PSDB: AAY58184.
XX
PT Recombinant fowlpox virus useful as a vaccine for immunizing fowl
PT against Marek's disease, Newcastle disease, Infectious
PT Laryngotracheitis virus and/or Fowlpox
XX
PS Claim 5; Columns 77-80; 56pp; English.
XX
CC The invention relates to a recombinant fowlpox virus (FPV)
CC comprising a foreign DNA inserted into a 4.2 kb EcoRI fragment
CC of the fowlpox virus genome. The foreign DNA is capable of being
CC expressed in a host cell into which the fowlpox virus has been
CC introduced and encodes an antigenic protein. The antigenic protein
CC which may be expressed includes infectious laryngotracheitis virus
CC (ILTV) glycoprotein B (gp) or glycoprotein D (gp; AAY58184), Newcastle
CC disease virus (NDV) haemagglutinin (HN; AAY58182) or fusion (F) protein

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CC (AAV5183) and Marek's disease virus gB or gD. The foreign DNA may
 CC alternatively encode a cytokine such as chicken myelomonocytic growth
 CC factor (CMGF) or chicken interleukin (cILFN). The foreign DNA in the
 CC recombinant FPV is under the control of one or more synthetic pox
 CC promoters, enabling control of strength and timing of heterologous
 CC gene expression. The synthetic pox virus promoters that may be used are
 CC based on promoters of the vaccinia virus and include early promoter 1
 CC (EP1), late promoter 1 (LP1), EP2 and LP2 (AA749291-249294,
 CC respectively). The recombinant FPV is generated via homologous
 CC recombination between FPV DNA and a homology vector containing the
 CC foreign DNA flanked by FPV sequences. The recombinant fowlpox viruses of
 CC the invention are used as multivalent live vaccines for immunising fowl
 CC against Marek's disease virus, NDV, ILTV and/or fowlpox virus. The
 CC present sequence represents the ILTV glycoprotein D (gD) gene.
 xx

Sequence 1305 BP, 331 A, 349 C, 344 G, 281 T, 0 other;

Query Match Best Local Similarity 100.0%; Score 1305; DB 21; Length 1305;

Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCACGCTCCTCATCTCAGACGACCTCGCTACTACGCGAAGAGAGGCTTAAAC 60
 Db 1 ATGCACGCTCCTCATCTCAGACGACCTCGCTACTACGCGAAGAGAGGCTTAAAC 60
 QY 61 AAACACATGATTCGCGTGGAAAACGCTGCTCAGGCGCAGCTGATTCACCTTTTC 120
 Db 61 AAACACATGATTCGCGTGGAAAACGCTGCTCAGGCGCAGCTGATTCACCTTTTC 120
 QY 121 TGGACTGTGTCAGATTATTCGCGGAGCATATCTGCTTTGATGCAACGCTATGACCCG 180
 Db 121 TGGACTGTGTCAGATTATTCGCGGAGCATATCTGCTTTGATGCAACGCTATGACCCG 180
 QY 181 CATTATTTTGGAGAAATGCTTTTGGACTATGCTACTGCTTCTTCTCGCTAGGACG 240
 Db 181 CATTATTTTGGAGAAATGCTTTTGGACTATGCTACTGCTTCTTCTCGCTAGGACG 240
 QY 241 AGCACGCGCGCGCTACGCTACGCTACATTTTACGCCGTGCGCGCTGACGCGCTAAC 300
 Db 241 AGCACGCGCGCGCTACGCTACGCTACATTTTACGCCGTGCGCGCTGACGCGCTAAC 300
 QY 301 ATACCGCGGCTGCGCGCTATACAGATACCTACCTAGGCTATCAAGAGGCTGCGACG 360
 Db 301 ATACCGCGGCTGCGCGCTATACAGATACCTACCTAGGCTATCAAGAGGCTGCGACG 360
 QY 361 GTGAGCTCAGCCGATTTTAACTGAGAGCATATATGCGCGCCAAAGAAAAGAG 420
 Db 361 GTGAGCTCAGCCGATTTTAACTGAGAGCATATATGCGCGCCAAAGAAAAGAG 420
 QY 421 AAGGGGGGCGCTTTCAGAGCGCTCGTCTGCTGCTTACGCTATTAAGGGGCGACGCG 480
 Db 421 AAGGGGGGCGCTTTCAGAGCGCTCGTCTGCTGCTTACGCTATTAAGGGGCGACGCG 480
 QY 481 GAGGACAACTACTGCTCAATCTATAGAAAAGATACAGGGAATGUGGCGACGTACA 540
 Db 481 GAGGACAACTACTGCTCAATCTATAGAAAAGATACAGGGAATGUGGCGACGTACA 540
 QY 541 CTATTCGAATGGCGGCTGAATCTGACAGATGTGGGCGATGATGTTCTTAGAC 600
 Db 541 CTATTCGAATGGCGGCTGAATCTGACAGATGTGGGCGATGATGTTCTTAGAC 600
 QY 601 CTGTATTCGCGAAGATGGCGGAGCTGACTATATCTCCGACAGCTGCGCTCTG 660
 Db 601 CTGTATTCGCGAAGATGGCGGAGCTGACTATATCTCCGACAGCTGCGCTCTG 660
 QY 661 CAATACCTGCTGACCTGAAATCGGAGATTGCGCAACGCTCTGTAACCTAGAA 720
 Db 661 CAATACCTGCTGACCTGAAATCGGAGATTGCGCAACGCTCTGTAACCTAGAA 720
 QY 721 GTTAAAGATCGCTGTTTAAAGATCGGGGTGCGAGCTTAACTTTTACCGTGAATG 780
 Db 721 GTTAAAGATCGCTGTTTAAAGATCGGGGTGCGAGCTTAACTTTTACCGTGAATG 780

QY 781 ACAACAGACAGTATTCAGACTGATTTTCAAGGCGAACACCTTTATCGATCGACAC 840
 Db 781 ACAACAGACAGTATTCAGACTGATTTTCAAGGCGAACACCTTTATCGATCGACAC 840
 QY 841 AATACAGACAGCGGCGACGATATTCGGGTAGAGATATTTTTCGAGCGCTGGAAT 900
 Db 841 AATACAGACAGCGGCGACGATATTCGGGTAGAGATATTTTTCGAGCGCTGGAAT 900
 QY 901 AATTTGCTGAGAAAAGAAATCTAGCGCGCCAGACCTCTGTCAGATAGCGTCCGCA 960
 Db 901 AATTTGCTGAGAAAAGAAATCTAGCGCGCCAGACCTCTGTCAGATAGCGTCCGCA 960
 QY 961 GAATTTCCCTCTTACCAAGAAAGCGGAGAGGCGCACCCCGGACGCAAGAACG 1020
 Db 961 GAATTTCCCTCTTACCAAGAAAGCGGAGAGGCGCACCCCGGACGCAAGAACG 1020
 QY 1021 AAGAAGCCCTCTCAGACAGCTGAGAGACGACATCGAGAGGCTCTGAGAGAAAT 1080
 Db 1021 AAGAAGCCCTCTCAGACAGCTGAGAGACGACATCGAGAGGCTCTGAGAGAAAT 1080
 QY 1081 CCTGCGCGCTCCCGCAAGACGAGAGTCCCGAGGACACCGAGACGATGATCCAA 1140
 Db 1081 CCTGCGCGCTCCCGCAAGACGAGAGTCCCGAGGACACCGAGACGATGATCCAA 1140
 QY 1141 TCGATCTGACATATTCAGATGACGCGCGCGGATCCGCTGAGAGAGCTACTAA 1200
 Db 1141 TCGATCTGACATATTCAGATGACGCGCGCGGATCCGCTGAGAGAGCTACTAA 1200
 QY 1201 AGTTCTAATGCGCTCTCATGCGCCATATTCGCGGCTTGTGATGCGCGCTGCG 1260
 Db 1201 AGTTCTAATGCGCTCTCATGCGCCATATTCGCGGCTTGTGATGCGCGCTGCG 1260
 QY 1261 GTGGGCTACTGCTTGGAGCATCGTAATATCGCGGCTGACTAA 1305
 Db 1261 GTGGGCTACTGCTTGGAGCATCGTAATATCGCGGCTGACTAA 1305

RESULT 6
 AAT33504
 ID AAT33504 standard; DNA; 13473 BP.

AC AAT33504;
 XX 18-NOV-1996 (first entry)
 DF
 DE Infectious laryngotracheitis virus short region sequence.
 XX Infectious laryngotracheitis virus; ILTV; herpesvirus;
 KW attenuation; vector; vaccine; chicken; poultry; immunisation; ds.
 OS Infectious laryngotracheitis virus.
 XX
 FH
 FH Key location/Qualifiers
 FT repeat_region 1..273
 FT /tag= a
 FT /function= internal repeat region
 FT misc_feature 274..13371
 FT /tag= b
 FT /function= unique short sequence of ILTV
 FT CDS complement (281..970)
 FT /tag= c
 FT /label= US2_gene
 FT 1059..2489
 FT /tag= d
 FT /label= Protein-kinase_gene
 FT 2575..4107
 FT /tag= e
 FT /label= UL47-like_gene
 FT 4113..4445
 FT /tag= f
 FT /label= ORF4
 FT complement (4139..4519)
 FT /tag= g
 FT CDS

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FT      /label= DRF4_reverse_complement
FT      4535
FT      /tag= h
FT      /note= "base 4535 is given as 's' in the
FT      specification"
FT      CDS
FT      4609..5487
FT      /tag= i
FT      /label= gg_gene
FT      5697..8654
FT      /tag= j
FT      /label= g60_gene
FT      complement (6948..7826)
FT      CDS
FT      /tag= k
FT      /label= ORF6_reverse_complement
FT      8462..9766
FT      /tag= l
FT      /label= gd_gene
FT      9874..10962
FT      CDS
FT      /tag= m
FT      /label= gi_gene
FT      complement (10617..11150)
FT      CDS
FT      /tag= n
FT      /label= ORF8_reverse_complement
FT      11159..12658
FT      /tag= o
FT      /label= ge_gene
FT      12665..13447
FT      /tag= p
FT      /label= DRF10
FT      misc_difference 13002..13303
FT      /tag= q
FT      /note= "bases 13002-13303 are given as 'ss' in
FT      the specification"
FT      repeat_region
FT      13372..13473
FT      /tag= r
FT      /function= terminal repeat region
FT      W09508622-A1.
XX
XX      30-MAR-1995.
XX
XX      16-SEP-1994: 94WO-US10628.
XX
XX      24-SEP-1993: 93US-0126597.
XX
XX      (SYTR ) SYNTRD CORP.
XX
XX      Cochran MD, WILD MA;
XX
XX      WPI: 1995-139591/18.
XX      P-PSDB: AAM00630, AAM00631, AAM00632, AAM00633, AAM00634, AAM00635,
XX      AAM00636, AAM00637, AAM00638, AAM00639, AAM00640, AAM00641 W00642.
XX
XX      Recombinant attenuated infectious laryngotracheitis virus - for use
XX      in vaccines to protect poultry from infection from the virus, also
XX      methods of distinguishing between vaccinated and naturally infected
XX      birds
XX
XX      Example 1: Page 79-94, 177pp: English.
XX
XX      The unique short region (AAT33504) of infectious laryngotracheitis
XX      virus (ILTV) genomic DNA contains genes (see also AAT33505 and
XX      AAT33510-13) that are associated with ILTV virulence. A deletion in
XX      those genes, esp. the glycoprotein gg gene, glycoprotein gi gene,
XX      thymidine kinase gene, uS2 gene, uI47-like gene or the glycoprotein
XX      g60 gene, will attenuate the ILTV. A gene for a foreign antigen may
XX      be inserted into the uS2, uI47-like, DRF4, gg, g60 or gi gene to
XX      produce a recombinant ILTV. Recombinant ILTV may be used as a
XX      multivalent vaccine, esp. for use in poultry.
XX
XX      Sequence 13473 BP; 3390 A; 3582 C; 3547 G; 2951 T; 3 other:
XX
XX      Query Match 100.0%; Score 1305; DB 16; Length 13473;
```

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGCACGCTCTCATCTTCAGACGCACTCGCGTTACTACGGAAGAGAGGTCTTAAC 60
DB      |||||||
DB      8462 ATGCACGCTCTCATCTTCAGACGCACTCGCGTTACTACGGAAGAGAGGTCTTAAC 8521
QY      61 AAACACATGATTTGCGGTGGGAAAAAGGTGCTCAGGCGGAGGTGATTACCTTTTC 120
DB      |||||||
DB      8522 AAACACATGATTTGCGGTGGGAAAAAGGTGCTCAGGCGGAGGTGATTACCTTTTC 8581
QY      121 TGGACTGTGTGACGATTTATCGGGAGCAATATGCTTTTGTACCAACGCTATGACCGC 180
DB      |||||||
DB      8582 TGGACTGTGTGACGATTTATCGGGAGCAATATGCTTTTGTACCAACGCTATGACCGC 8641
QY      181 CATTATTTTGGAGAAATGCTTTTGGACTATCTGACTGCTTCTTCTTCGTACGACAG 240
DB      |||||||
DB      8642 CATTATTTTGGAGAAATGCTTTTGGACTATCTGACTGCTTCTTCTTCGTACGACAG 8701
QY      241 AGCACCGCGCGCTTCACGATGACTTACATTTTAAAGCGGCGGCTGACGCGCTAAC 300
DB      |||||||
DB      8702 AGCACCGCGCGCTTCACGATGACTTACATTTTAAAGCGGCGGCTGACGCGCTAAC 8761
QY      301 ATACCGGGGCTTGGCCGCTATACAGATACCTCTACTAGGGATCAAGAGGCTGGACGTT 360
DB      |||||||
DB      8762 ATACCGGGGCTTGGCCGCTATACAGATACCTCTACTAGGGATCAAGAGGCTGGACGTT 8821
QY      361 GTCGAGCTCAACCGGATTTTCACTGACGACATGATATTCGGGCGCAAAAGAAAGAG 420
DB      |||||||
DB      8822 GTCGAGCTCAACCGGATTTTCACTGACGACATGATATTCGGGCGCAAAAGAAAGAG 8881
QY      421 AAGGGGGCCCTTTCGAGGCGCTCGTGTCTGTTTACGTGATTAAGGCGAGACGGC 480
DB      |||||||
DB      8882 AAGGGGGCCCTTTCGAGGCGCTCGTGTCTGTTTACGTGATTAAGGCGAGACGGC 8941
QY      481 GAGGACAAGTACGTCTCAATCTATAGAAAGAGTACAGGGAATGGCGACGTACAAC 540
DB      |||||||
DB      8942 GAGGACAAGTACGTCTCAATCTATAGAAAGAGTACAGGGAATGGCGACGTACAAC 9001
QY      541 CTATCTGAATGCGCGCTTTCATCTGCACAGATGTGGGCGAGTGTATGTTCTAGACAC 600
DB      |||||||
DB      9002 CTATCTGAATGCGCGCTTTCATCTGCACAGATGTGGGCGAGTGTATGTTCTAGACAC 9061
QY      601 CTTGTATCGGAAATGCGCGGCGAGTACTATATTTCTCCCCACTGCTGCGCTCTGGC 660
DB      |||||||
DB      9062 CTTGTATCGGAAATGCGCGGCGAGTACTATATTTCTCCCCACTGCTGCGCTCTGGC 9121
QY      661 CAATACCTTGTGACCCCTGAAATATGCGGAGATTTGCGCAACAGTCTCGTACTGTAGAA 720
DB      |||||||
DB      9122 CAATACCTTGTGACCCCTGAAATATGCGGAGATTTGCGCAACAGTCTCGTACTGTAGAA 9181
QY      721 GTTACGATGCGCTTTTAAAGATGCGGTCCAGCTTAACTTTTACCGTGAATGCTGG 780
DB      |||||||
DB      9182 GTTACGATGCGCTTTTAAAGATGCGGTCCAGCTTAACTTTTACCGTGAATGCTGG 9241
QY      781 ACAACAGACAGTATCAGACTGATTTCAAGCGGACACCTTTATCCGATCGACACACC 840
DB      |||||||
DB      9242 ACAACAGACAGTATCAGACTGATTTCAAGCGGACACCTTTATCCGATCGACACACC 9301
QY      841 AATACAGACAGCGGCGGAGCGATATTCGGGGATACGAATATTCGCGACGCGCTGGAAT 900
DB      |||||||
DB      9302 AATACAGACAGCGGCGGAGCGATATTCGGGGATACGAATATTCGCGACGCGCTGGAAT 9361
QY      901 AATTGTGTAGAAAAAAGATTCCTAGCGCCACAGACCTCTGTCAGATACGTCGCGCAA 960
DB      |||||||
DB      9362 AATTGTGTAGAAAAAAGATTCCTAGCGCCACAGACCTCTGTCAGATACGTCGCGCAA 9421
QY      961 GAAATTCGCGCTGTACCAAGAAAGCGGAAGGCGCACCCCGGACGCAAGAACGAGGAA 1020
DB      |||||||
DB      9422 GAAATTCGCGCTGTACCAAGAAAGCGGAAGGCGCACCCCGGACGCAAGAACGAGGAA 9481
QY      1021 AAGAGGCGCCTCGAGAAAGCTCGGAGGAGACATGAGGCGAAGGCTTGTGAGAAAT 1080
DB      |||||||
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Db 9482 AAGAGGCCCTCCAGAGACTCGAGAGACATGACAGCGAGAGCTTCGAGAGAAAT 9541
Qy 1081 COTGCCGCCCTCCCGAGAGACGAGACTCCCGGAGACACCGACAGATGATCCAAAC 1140
Db 9542 CCTGCCGCCCTCCCGAGAGACGAGACTCCCGGAGACACCGACAGATGATCCAAAC 9601
Qy 1141 TCGGATCCTGACTATTACAAATGACATGCCGCCGCTGATCCGGTGGAGAGACTACTAAA 1200
Db 9602 TCGGATCCTGACTATTACAAATGACATGCCGCCGCTGATCCGGTGGAGAGACTACTAAA 9661
Qy 1201 AGTTCTAATGCGCTGCATGCGCCATATTCGCGCGCTTCGTAAGCCTGCGCGCTGCCTC 1260
Db 9662 AGTTCTAATGCGCTGCATGCGCCATATTCGCGCGCTTCGTAAGCCTGCGCGCTGCCTC 9721
Qy 1261 GTGGGGCTACTGTTTGGAGCATGCTAAATGCGCGCTACTCTAA 1305
Db 9722 GTGGGGCTACTGTTTGGAGCATGCTAAATGCGCGCTACTCTAA 9766

RESULT 7
AAT44384
ID AAT44384 standard; DNA: 13473 BP.
XX
AC AAT44384;
XX
DT 02-JUN-1997 (first entry)
XX
DE Infectious laryngotracheitis virus unique short region.
XX
KW ILTV; vaccine; vector; attenuation; poultry;
KW avian infectious bronchitis virus; Newcastle disease virus;
KW infectious bursal disease virus of chickens;
KW Marek's disease virus; herpesvirus; ss.
XX
OS Infectious laryngotracheitis virus USDA strain 8302.
XX
FH Key Location/Qualifiers
FT repeat_region 1..273
FT msc_RNA 274..13371
FT polyA_signal 161..166
FT CDS /note= "polyA signal for ORF1"
FT /tag= c
FT /label= ORF1(RC)
FT /note= "unique-like short 2 (US2) gene"
FT TATA_signal 1007..1010
FT /tag= e
FT /note= "TATA signal for ORF1 and ORF2"
FT TATA_signal 1040..1043
FT /tag= f
FT /note= "TATA signal for ORF1"
FT TATA_signal 1042..1045
FT /tag= g
FT /note= "TATA signal for ORF2"
FT CDS /note= "TATA signal for ORF2"
FT /tag= h
FT /label= ORF2
FT /note= "protein kinase gene"
FT polyA_signal 2491..2496
FT /tag= i
FT /note= "polyA signal for ORF2"
FT polyA_signal 2538..2543
FT /tag= j
FT /note= "polyA signal for ORF2"
FT CDS /note= "TATA signal for ORF2"
FT /tag= k
FT /label= ORF3
FT /note= "unique long 47 (UL47)-like gene"
FT TATA_signal 4523..4526
FT
FT /tag= 1
FT /note= "TATA signal for ORF4"
FT CDS 4113..4445
FT /tag= m
FT /label= ORF4
FT CDS complement (4139..4519)
FT /tag= n
FT /label= ORF4(RC)
FT TATA_signal 4523..4526
FT /tag= o
FT /note= "TATA signal for ORF5"
FT CDS 4609..5487
FT /tag= p
FT /label= ORF5
FT sig_peptide 4609..4686
FT /tag= q
FT mat_peptide 4687..5484
FT polyA_signal 5564..5569
FT /tag= s
FT /note= "polyA site for ORF5"
FT polyA_signal 5653..5658
FT /tag= t
FT /note= "polyA signal for ORF5"
FT CDS 5697..8654
FT /tag= u
FT /label= ORF6
FT repeat_region 6987..7727
FT /tag= v
FT /note= "repeat region consists of approx. 23
FT /note= "repeats of 30-36 bp"
FT CDS complement (6948..7826)
FT /tag= w
FT /label= ORF6(RC)
FT TATA_signal 8455..8458
FT /tag= x
FT /note= "potential TATA signal for ORF7"
FT CDS 8461..9766
FT /tag= y
FT /label= ORF7
FT /note= "glycoprotein gD gene, alternative start
FT /note= "codon at 8633..8635"
FT TATA_signal 9819..9822
FT /tag= z
FT /note= "TATA signal for ORF8"
FT CDS 9874..10962
FT /tag= aa
FT /label= ORF8
FT /note= "glycoprotein gI gene"
FT sig_peptide 9874..9939
FT /tag= ab
FT mat_peptide 9940..10959
FT /tag= ac
FT CDS complement (10617..11150)
FT /tag= ad
FT /label= ORF8(RC)
FT TATA_signal 11069..11072
FT /tag= ae
FT /note= "TATA signal for ORF9"
FT CDS 11159..12658
FT /tag= af
FT /label= ORF9
FT /note= "glycoprotein gE gene"
FT sig_peptide 11159..11212
FT /tag= ag
FT mat_peptide 11213..12655
FT /tag= ah
FT TATA_signal 12483..12486
FT /tag= ai
FT /note= "TATA signal for ORF10"
FT CDS 12665..13447

```

```
FT      /*lag- aJ
FT      /label- ORF10
FT      repeat_region 13372..13743
FT      /*lag- ak
PN      MO9629396-A1.
XX
XX      26-SEP-1996.
XX
XX      21-MAR-1996: 96WO-US03916.
XX
XX      06-JUN-1995: 95US-0468190.
XX      23-MAR-1995: 95US-0410121.
XX
XX      (SYTR ) SYNTRO CORP.
XX      Cochran MD, Wild MA;
XX
XX      WPI: 1996-443172/44.
XX      P-PSDB: AAM06782;
XX      P-PSDB: AAM06783;
XX      P-PSDB: AAM06784;
XX      P-PSDB: AAM06785;
XX      P-PSDB: AAM06786;
XX      P-PSDB: AAM06787;
XX      P-PSDB: AAM06788;
XX      P-PSDB: AAM06789;
XX      P-PSDB: AAM06790;
XX      P-PSDB: AAM06791;
XX      P-PSDB: AAM06792;
XX      P-PSDB: AAM06793.
XX
XX      Recombinant infectious laryngotracheitis virus with deletion in the
XX      glycoprotein G, g1 or US2 gene, etc. - useful for vaccines against
XX      infectious laryngotracheitis in poultry
XX
XX      Example 11: Page 88-103; 216pp; English.
XX
XX      The nucleotide sequence of 13,473 bp of contiguous DNA (AAT44384)
XX      from the unique short region of infectious laryngotracheitis virus
XX      (ILTV) contains the entire 13,098 bp unique short region and
XX      includes 13 open reading frames that encode proteins (AAM06782-94) of
XX      over 100 amino acids, 8 of which show significant homology to other
XX      CC virus genes. Novel recombinant, attenuated ILTV comprises the ILTV
XX      genome contg. a deletion in the unique short region, esp. in the
XX      glycoprotein g6, g1, US2, ORF4, UL47-like or g60 gene. The
XX      CC attenuated virus is useful as a vaccine against ILTV. A foreign
XX      CC gene encoding an antigen e.g. from another avian virus can be
XX      CC inserted into the US2, UL47-like, ORF4, g6, g60 or g1 gene to
XX      CC provide a multivalent vaccine for chickens and other poultry.
XX      CC Deletion of the g6 or g1 gene provides as a negative marker to
XX      CC distinguish vaccinated from infected animals.
XX
XX      Sequence 13473 BP; 3390 A; 3581 C; 3547 G; 2952 T; 3 other:
XX
XX      Query Match      100.0%; Score 1305; DB 17; Length 13473;
XX      Best Local Similarity 100.0%; Pred. No. 0;
XX      Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Db      8642 CATTATTTTGGAGAAATGCTTTTGGACTATGCTACTGCTTCTTCTGCTAGGCAG 8701
QY      AGACACCGCCGCGTACAGTACGACTACATTTTAAAGCGGTGCGGCTGACGCGCTAAC 300
Db      8702 AGCACCCCGCGCTACAGTACGACTACATTTTAAAGCGGTGCGGCTGACGCGCTAAC 8761
QY      301 ATTACGGCGGTGGCCCGCTAATACAGATACCTCACTAGGGATATACAGAGCTGGAGCTT 360
Db      8762 ATTACGGCGGTGGCCCGCTAATACAGATACCTCACTAGGGATATACAGAGCTGGAGCTT 8821
QY      361 GTCGAGCTCAACCGATTTTCAAGTACGACATGATATATGCGCGCCAAAGAAAGAG 420
Db      8822 GTCGAGCTCAACCGATTTTCAAGTACGACATGATATATGCGCGCCAAAGAAAGAG 8881
QY      421 AAGGGGGGCCCTTTGAGAGCCCTCGTGTGTTTACGTGATTAAGGCGAGCAGGC 480
Db      8882 AAGGGGGGCCCTTTGAGAGCCCTCGTGTGTTTACGTGATTAAGGCGAGCAGGC 8941
QY      481 GAGGACAAGTACGCTCCATCTATAGAAAGAGTACAGAGGAATGGCGAGCTCAACTG 540
Db      8942 GAGGACAAGTACGCTCCATCTATAGAAAGAGTACAGAGGAATGGCGAGCTCAACTG 9001
QY      541 CTATCTGAATGCGCGCTTCAATCTGACAGATGTGGGAGTGAAGTATGTTCTAGACAC 600
Db      9002 CTATCTGAATGCGCGCTTCAATCTGACAGATGTGGGAGTGAAGTATGTTCTAGACAC 9061
QY      601 CTTGTATCGGGAATGCGCGGAGTACTATATATTCGCCACTGCTGCGCTCTGCG 660
Db      9062 CTTGTATCGGGAATGCGCGGAGTACTATATATTCGCCACTGCTGCGCTCTGCG 9121
QY      661 CAATACTGCTGACACCCGAAATGGGAGATTTGCGCAACAGCTCTGTAATCTTGAA 720
Db      9122 CAATACTGCTGACACCCGAAATGGGAGATTTGCGCAACAGCTCTGTAATCTTGAA 9181
QY      721 GTTACGATGCTGTTTAAAGATGCGTCACTTATCTTACCGTGAATGCTGG 780
Db      9182 GTTACGATGCTGTTTAAAGATGCGTCACTTATCTTACCGTGAATGCTGG 9241
QY      781 ACAACAGACAGTATGACAGTGTTCAAAGCGACACCTTTATCCGATCGACAGACC 840
Db      9242 ACAACAGACAGTATGACAGTGTTCAAAGCGACACCTTTATCCGATCGACAGACC 9301
QY      841 AATACAGACAGCGGAGCGAGTATATCGGGGATACGAAGATNTTTCAGCGCTGGAAT 900
Db      9302 AATACAGACAGCGGAGCGAGTATATCGGGGATACGAAGATNTTTCAGCGCTGGAAT 9361
QY      901 AATTTGCTGAGAAAGAAATCTAGCGCGCCAGACCCCTGTCAGATATAGCTCCGCAA 960
Db      9362 AATTTGCTGAGAAAGAAATCTAGCGCGCCAGACCCCTGTCAGATATAGCTCCGCAA 9421
QY      961 GAAATTCGCGCTGTACCAAGAAAGCGGAGCGCACCCCGGACGAGAAAGCAGCGAA 1020
Db      9422 GAAATTCGCGCTGTACCAAGAAAGCGGAGCGCACCCCGGACGAGAAAGCAGCGAA 9481
QY      1021 AAGAGGCGCCCTCAGAAAGACTGGAGAGACATGAGAGGAGAGGCTTTGGGAAAT 1080
Db      9482 AAGAGGCGCCCTCAGAAAGACTGGAGAGACATGAGAGGAGAGGCTTTGGGAAAT 9541
QY      1081 CTTGCCGCCCTCCCGAAGAGCAGAAAGTCCCGAGAGACACCGACAGATGATCCAAAC 1140
Db      9542 CTTGCCGCCCTCCCGAAGAGCAGAAAGTCCCGAGAGACACCGACAGATGATCCAAAC 9601
QY      1141 TCGGATCTGACTATTAATCAATGACATGCGCGCTGATCCCGGTGAGAGACTACTAAA 1200
Db      9602 TCGGATCTGACTATTAATCAATGACATGCGCGCTGATCCCGGTGAGAGACTACTAAA 9661
QY      1201 AGTTCTAATGCGCTTCATGAGCCCATATTTGCGGCGTGTCTAGCTGCGCGGCTC 1260
Db      9662 AGTTCTAATGCGCTTCATGAGCCCATATTTGCGGCGTGTCTAGCTGCGCGGCTC 9721
QY      1261 GTGGGGCTACTGTTTGGAGCATGTAAATGCGCGGTGTAGCTAA 1305
Db      9722 GTGGGGCTACTGTTTGGAGCATGTAAATGCGCGGTGTAGCTAA 9766
```

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RESULT 8
AAT44385
ID AAT44385 standard; DNA; 18912 BP.
XX
AC AAT44385;
XX
DT 02-JUN-1997 (first entry)
XX
XX Infectious laryngotracheitis virus unique short + flanking region.
XX
XX ILTV; vaccine; vector: attenuation; poultry;
XX avian infectious bronchitis virus; Newcastle disease virus;
XX infectious bursal disease virus of chickens;
XX Marek's disease virus; herpesvirus; ss.
XX
OS Infectious laryngotracheitis virus USDA strain 8302.
XX
FH Key Location/Qualifiers
FT repeat_region 1..2909
FT /*tag= a
FT /note= "short repeat region"
FT 697..1533
FT /*tag= b
FT /label= "SRORF2"
FT /note= "US10 gene"
FT complement (2916..3605)
FT /*tag= c
FT /label= "SRORF1"
FT /note= "short repeat open reading frame 1"
FT 2910..16003
FT /*tag= d
FT /note= "unique short region"
FT 2796..2891
FT /*tag= e
FT /note= "polyA signal for ORF1"
FT complement (2916..3605)
FT /*tag= f
FT /label= "ORF1(RC)"
FT /note= "unique-like short 2 (US2) gene"
FT 3642..3645
FT /*tag= g
FT /note= "TATA signal for ORF1 and ORF2"
FT 3675..3678
FT /*tag= h
FT /note= "TATA signal for ORF1"
FT 3677..3680
FT /*tag= i
FT /note= "TATA signal for ORF2"
FT 3694..5124
FT /*tag= j
FT /label= "ORF2"
FT /note= "protein kinase gene"
FT 5126..5131
FT /*tag= k
FT /note= "polyA signal for ORF2"
FT 5173..5178
FT /*tag= l
FT /note= "polyA signal for ORF2"
FT 5210..7081
FT /*tag= m
FT /label= "ORF3"
FT /note= "unique long 47 (UL47)-like gene"
FT 7158..7161
FT /*tag= n
FT /note= "TATA signal for ORF4"
FT 6748..7080
FT /*tag= o
FT /label= "ORF4"
FT complement (6774..7154)
FT /*tag= p
FT /label= "ORF4(RC)"

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FT TATA_signal 7158..7161
FT /*tag= g
FT /note= "TATA signal for ORF5"
FT 7245..8123
FT /*tag= r
FT /label= "ORF5"
FT /note= "glycoprotein g6 gene"
FT 7245..7322
FT /*tag= s
FT 7323..8120
FT /*tag= t
FT 8200..8205
FT /*tag= u
FT /note= "polyA site for ORF5"
FT 8289..8294
FT /*tag= v
FT /note= "polyA signal for ORF5"
FT 8333..11290
FT /*tag= w
FT /label= "ORF6"
FT /note= "glycoprotein g60 gene"
FT 9623..10363
FT /*tag= x
FT /note= "repeat region consists of approx. 23
FT repeats of 30-36 bp"
FT complement (9584..10462)
FT /*tag= y
FT /label= "ORF6(RC)"
FT 11091..11094
FT /*tag= z
FT /note= "potential TATA signal for ORF7"
FT 11098..12402
FT /*tag= aa
FT /label= "ORF7"
FT 12455..12448
FT /*tag= ab
FT /note= "TATA signal for ORF8"
FT 12510..13598
FT /*tag= ac
FT /label= "ORF8"
FT /note= "glycoprotein gi gene"
FT 12510..12575
FT /*tag= ad
FT 12576..13595
FT /*tag= ae
FT complement (13253..13786)
FT /*tag= af
FT /label= "ORF8(RC)"
FT 13705..13708
FT /*tag= ag
FT /note= "TATA signal for ORF9"
FT 13792..15291
FT /*tag= ah
FT /label= "ORF9"
FT /note= "glycoprotein g6 gene"
FT 13792..13845
FT /*tag= ai
FT 13846..15288
FT /*tag= aj
FT 15116..15119
FT /*tag= ak
FT /note= "TATA signal for ORF10"
FT 15298..16080
FT /*tag= al
FT /label= "ORF10"
FT 16004..18912
FT /*tag= am
FT 16129..17013
FT /*tag= an
FT complement (17380..18216)
FT /*tag= ao
XX
XX WO9629396-A1.
PN

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XX 26-SEP-1996.
PD
XX
XX 21-MAR-1996; 96WQ-US03916.
PF
XX
PR 06-JUN-1995; 95US-0468190.
PR 23-MAR-1995; 95US-0410121.
XX
PA (SYTR ) SYNTRO CORP.
XX
XX Cochran MD, Wild MA;
XX
XX WPI: 1996-443172/44.
DR P-RSDs: AAM06782, AAM06783, AAM06784, AAM06785, AAM06786, AAM06787,
DR AAM06788, AAM06789, AAM06790, AAM06791, AAM06792, AAM06793, AAM01415,
DR AAM01416.
XX
XX Recombinant infectious laryngotracheitis virus with deletion in the
PT glycoprotein G, gI or uS2 gene, etc. - useful for vaccines against
PT infectious laryngotracheitis in poultry
XX
XX Example 11; Page 138-154; 216pp, English.
XX
XX The nucleotide sequence of 19,912 bp of contiguous DNA (AAT44385)
CC from the unique short and flanking region of infectious
CC laryngotracheitis virus (ILTV) contains the entire 13,098 bp unique
CC short region (see also AAT44384) and includes 17 open reading frames
CC that encode proteins (AAM06782-94, AAM01415-16) of over 100 amino
CC acids, 10 of which show homology to other virus genes. Novel
CC recombinant, attenuated ILTV comprises the ILTV genome contg. a
CC deletion in the unique short region, esp. in the glycoprotein gG,
CC gI, uS2, ORF4, UL47-like or g60 gene. The attenuated virus is
CC useful as a vaccine against ILTV. A foreign gene encoding an
CC antigen e.g. from another avian virus can be inserted into the uS2,
CC UL47-like, ORF4, g6, g60 or gI gene to provide a multivalent
CC vaccine for chickens and other poultry. Deletion of the gG or gI
CC gene provides as a negative marker to distinguish vaccinated from
CC infected animals.
XX
XX Sequence 18912 BP; 4416 A; 5261 C; 5251 G; 3984 T; 0 other:
SO
Query Match 100.0%; Score 1305; DB 17; Length 18912;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGCACGCTCTCATCTAGACGCGACTGCGTTACTACGCGAAGAGAGAGCTTTTAC 60
DB 11098 ATGCACGCTCTCATCTAGACGCGACTGCGTTACTACGCGAAGAGAGAGCTTTTAC 11537
OY 61 AAMCAGATGATGGGGAAGAAAGCGTGTCTGTCAGGCGAGCTGATTCACCTTTTC 120
DB 11158 AAMCAGATGATGGGGAAGAAAGCGTGTCTGTCAGGCGAGCTGATTCACCTTTTC 11217
OY 121 TGCAGTGTGTAGAGATTATCGGGAGCATATGCTTTGTACGCAACGCTATGAGCCG 180
DB 11218 TGCAGTGTGTAGAGATTATCGGGAGCATATGCTTTGTACGCAACGCTATGAGCCG 11217
OY 181 CATTTATTTTGGAGAAATGCTTTTGGACTATGCTACTGCTTTCTCTTCTGCTAGCCAG 240
DB 11278 CATTTATTTTGGAGAAATGCTTTTGGACTATGCTACTGCTTTCTCTTCTGCTAGCCAG 11337
OY 241 AGCAGCGCGCGCTGACGTACGACATCTTTAGCGCTGCGGCGCTGAGCGCTTACG 300
DB 11338 AGCAGCGCGCGCTGACGTACGACATCTTTAGCGCTGCGGCGCTGAGCGCTTACG 11337
OY 301 ATACCGGCGTTGGCCCTATACAGATACCTCACTAGAGTATCAAGAGCTGCGACGTT 360
DB 11398 ATACCGGCGTTGGCCCTATACAGATACCTCACTAGAGTATCAAGAGCTGCGACGTT 11457
OY 361 GTGAGCTCAACCGGATTTCTAACGTGAGACATGATATGGGCGCCAAAGAAAGAG 420
DB 11458 GTGAGCTCAACCGGATTTCTAACGTGAGACATGATATGGGCGCCAAAGAAAGAG 11517

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OY 421 AAGGGGGCCCTTTCGAGGCCCTCGCTGTTCTACGTATTAAGGGGAGACGGC 480
DB 11518 AAGGGGGCCCTTTCGAGGCCCTCGCTGTTCTACGTATTAAGGGGAGACGGC 11577
OY 481 GAGGACAGTACTGTCTCAATCTATAGAAAGAGTACAGGAGATGGGAGCTCAACTG 540
DB 11578 GAGGACAGTACTGTCTCAATCTATAGAAAGAGTACAGGAGATGGGAGCTCAACTG 11637
OY 541 CTATCTGAATGGCCGTTCAATCTGACAGATGTGGGAGTGGACTATGTTCTAGACC 600
DB 11638 CTATCTGAATGGCCGTTCAATCTGACAGATGTGGGAGTGGACTATGTTCTAGACC 11697
OY 601 CTGTATGCGCAAAATGGGCGGAGTGCATATTTCTCCCGACGCTGCGCTCAGC 660
DB 11698 CTGTATGCGCAAAATGGGCGGAGTGCATATTTCTCCCGACGCTGCGCTCAGC 11757
OY 661 CAATCTTGTGACCCCTGAAAATCGGAGATTGGCAAGACGCTCTGTAACCTAGAA 720
DB 11758 CAATCTTGTGACCCCTGAAAATCGGAGATTGGCAAGACGCTCTGTAACCTAGAA 11817
OY 721 GTTAACGATCGCTGTTAAAGTGGGTCGACGCTTAACCTTTTACCGTCAAAATGCTGG 780
DB 11818 GTTAACGATCGCTGTTAAAGTGGGTCGACGCTTAACCTTTTACCGTCAAAATGCTGG 11877
OY 781 ACAACAGAACAGTATCAGACTGATTTTCAGGCGAACCTTTATCCGATGCGACAGACC 840
DB 11878 ACAACAGAACAGTATCAGACTGATTTTCAGGCGAACCTTTATCCGATGCGACAGACC 11937
OY 841 AATACAGCAGACGGCGAGACGTATATGGGGATACGAAGATATTTGACGCGCTGAA 900
DB 11938 AATACAGCAGACGGCGAGACGTATATGGGGATACGAAGATATTTGACGCGCTGAA 11997
OY 901 AATTTGCTGAGAAAAAATCTTAGCCGCCAGACCCCTGCTCCAGATAGGCTCCCGAA 960
DB 11998 AATTTGCTGAGAAAAAATCTTAGCCGCCAGACCCCTGCTCCAGATAGGCTCCCGAA 12057
OY 961 GAATTTCCCGCTGTAAACAGAAAGCGGAGGCGCACCCCGGAGCGCAAGAAAGCGGAA 1020
DB 12058 GAATTTCCCGCTGTAAACAGAAAGCGGAGGCGCACCCCGGAGCGCAAGAAAGCGGAA 12117
OY 1021 AAGAAAGCCCTCCAGAAAGTCCGAGAGACATGACAGGAGGCTTTGAGAAAT 1080
DB 12118 AAGAAAGCCCTCCAGAAAGTCCGAGAGACATGACAGGAGGCTTTGAGAAAT 12177
OY 1081 CCTGCCGCCCTCCCGAAGAGAGCAAGTCCCGGAGGACACCGGACAGCATGATCCAAAC 1140
DB 12178 CCTGCCGCCCTCCCGAAGAGAGCAAGTCCCGGAGGACACCGGACAGCATGATCCAAAC 12237
OY 1141 TCGATCTCTGACTATTACATGACATGCGCCCGGTGATCCCGGTGAGAGACTACTTAA 1200
DB 12238 TCGATCTCTGACTATTACATGACATGCGCCCGGTGATCCCGGTGAGAGACTACTTAA 12297
OY 1201 AGTTCTAATGCCGCTCCATGCGCCCATATTCGCGGCGTTCTGAGCCTGCGCGCTC 1260
DB 12298 AGTTCTAATGCCGCTCCATGCGCCCATATTCGCGGCGTTCTGAGCCTGCGCGCTC 12357
OY 1261 GTGGGCGTACGTGTTTGGAGCATGCTAAATGGCGGCTACTTAA 1305
DB 12358 GTGGGCGTACGTGTTTGGAGCATGCTAAATGGCGGCTACTTAA 12402

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RESULT 9

AAQ22986 standard; DNA; 3502 BP.

AAQ22986;

02-NOV-1992 (first entry)

Sequence of ILTV gp60 gene.

Subunit vaccine; immunogen; glycoprotein; promoter; ss.

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OS Infectious laryngotracheitis virus.
XX Key Location/Qualifiers
FH TARA_signal 294..299
FT /*tag= a
FT 339..3326
FT /*tag= b
FT repeat_unit 1692..1712
FT /*tag= c
FT repeat_unit 1755..1775
FT /*tag= d
FT repeat_unit 1824..1841
FT /*tag= e
FT repeat_unit 1857..1871
FT /*tag= f
FT repeat_unit 1923..1943
FT /*tag= g
FT repeat_unit 1986..2006
FT /*tag= h
FT repeat_unit 2019..2039
FT /*tag= i
FT repeat_unit 2115..2129
FT /*tag= j
FT repeat_unit 2178..2198
FT /*tag= k
FT repeat_unit 2211..2228
FT /*tag= l
FT repeat_unit 2241..2261
FT /*tag= m
FT repeat_unit 2304..2324
FT /*tag= n
FT repeat_unit 2334..2351
FT /*tag= o
XX WO9203554-A.
XX PD 05-MAR-1992.
XX PE 23-AUG-1991; 91WO-AU00383.
XX PR 24-AUG-1990; 90AU-0001937.
XX PA (WEBS-) WEBSTER A PTY LTD.
XX PI Sheppard MG, Prideaux C, Johnson M, Fahey KJ, York JJ;
XX PI Kongsuwan K;
XX DX WPI; 1992-096898/12.
XX DR P-PSDB; AAR22234.
XX PT Vaccines against ILTV for use in chickens - comprises
XX PT non-infectious sub-units or live recombinant viruses and may be
XX PT administered by aerosol
XX PS Claim 14; Fig 6; 122pp; English.
XX
XX The inventors claim a non-infectious subunit vaccine for use against
XX ILTV which comprises a glycoprotein of ILTV. They also claim DNA
XX encoding the vaccine, a synthetic polypeptide displaying the
XX antigenicity of the 205k complex or 60k ILTV glycoprotein and a
XX recombinant ILTV with heterologous DNA inserted into a non-essential
XX region of the genome; and a recombinant DNA mol. comprising an ILTV
XX promoter region operatively linked to a heterologous DNA sequence.
XX or the ORF3 promoter region. Kpnk/ORF3 is located 5' of the gp60
XX gene. The deduced AA sequence of the gp60 gene has 19 hydrophobic
XX AA residues at the N-terminus which may correspond to the signal
XX sequence. A second region of hydrophobic AAs (posn. 960 to 989) at
XX the C-terminus could function as a transmembrane anchor sequence.
XX There are nine potential N-linked glycosylation sites on the ILTV
XX gp60 protein. One of these sites at residue 677, may not be active
XX due to the presence of a proline residue within the N-X-S/T signal.
XX There are repeated sequences within the ILTV gp60 coding region.

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CC They are not perfectly conserved but several copies had diverged so
CC that only 4 AAs out of 7 were conserved in all 13 copies of the
CC repeats. There is no significant homology between the protein and
CC any sequenced herpesvirus proteins in the database called PIR.
XX
XX Sequence 3502 BP; 845 A; 969 C; 920 G; 768 T; 0 other;
SO
Query Match 27.7%; Score 361; DB 13; Length 3502;
Best Local Similarity 98.6%; Pred. No. 2.1e-104;
Matches 364; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 ATGCACCGTCCTCATCTCAGACGCGCAGCTGCTACTACCGGAAAGAGAGTCTTAAC 60
DB 3134 ATGCACCGTCCTCATCTCAGACGCGCAGCTGCTACTACCGGAAAGAGAGTCTTAAC 3193
OY 61 AAACCATGATGATTCGCGTGGAAAAAGGTGCTCAGCGCAGCTGATTCACCTTTTC 120
DB 3194 GAACACATGATTCGCGTGGAAAAAGGTGCTCAGCGCAGCTGATTCACCTTTTC 3253
OY 121 TGGACTTGTGTGAGATTAATGCGGAGACATATCTGCTTTAGACCAAGCTATGACCGC 180
DB 3254 TGGACTTGTGTGAGATTAATGCGGAGACATATCTGCTTTAGACCAAGCTATGACCGC 3313
OY 181 CATTTATTTTGAAGAAATGCTTTTGGACTATGTAAGTCTTCTTCTTCTGCTAGCCAG 240
DB 3314 CATTTATTTTGAAGAAATGCTTTTGGACTATGTAAGTCTTCTTCTTCTGCTAGCCAG 3373
OY 241 AGCACGCGCCGCTCAGTACGACTATCTTTTGAAGCGCGCTGCGACGCTTAAC 300
DB 3374 AGCACGCGCCGCTCAGTACGACTATCTTTTGAAGCGCGCTGCGACGCTTAAC 3433
OY 301 ATACCGGCGGTTGGCCGTTAATACATACCTACTACTAGAGGTATCAAGAGGCTCCAGCTT 360
DB 3434 ATACCGGCGGTTGGCCGTTAATACATACCTACTACTAGAGGTATCAAGAGGCTCCAGCTT 3493
OY 361 GTCGAGCTC 369
DB 3494 GTCGAGCTC 3502
RESULT 10
AAT44399
ID AAT44399 standard; DNA; 42 BP.
XX
XX AC AAT44399;
XX
XX DT 03-JUN-1997 (first entry)
XX
XX DE Homology vector 562-61.1F junction B.
XX
XX ILTV; vaccine; homology vector 562-61.1F; attenuation; poultry;
XX avian infectious bronchitis virus; Newcastle disease virus;
XX infectious bursal disease virus of chickens;
XX Marek's disease virus; herpesvirus; glycoprotein 91; ss.
XX
XX Chimeric infectious laryngotracheitis virus.
XX
XX Key Location/Qualifiers
XX misc_RNA 1..24
XX /*tag= a
XX /*tag= b
XX /*tag= ILTV
XX /*tag= "3' end of approx. 1619 bp Asp7181-XbaI
XX /*tag= "5' end of approx. 691 bp XbaI-XhoI fragment
XX of ILTV, generated by PCR"
XX
XX misc_RNA 19..42
XX /*tag= b
XX /*tag= ILTV
XX /*tag= "5' end of approx. 691 bp XbaI-XhoI fragment
XX of ILTV, generated by PCR"
XX
XX MO9629396-A1.
XX 26-SEP-1996.

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XX 21-MAR-1996; 96WO-US03916.
PF
XX
XX 06-JUN-1995; 95US-0468190.
PR
XX 23-MAR-1995; 95US-0410121.
PR
XX
XX (SYTR ) SYNTRIO CORP.
PA
XX
XX Cochran MD, Wild MA;
PI
XX
XX WPI: 1996-443172/44.
DR
XX
XX Recombinant infectious laryngotracheitis virus with deletion in the
PT glycoprotein G, gI or uS2 gene, etc. - useful for vaccines against
PT infectious laryngotracheitis in poultry
XX
XX
XX Example 4; Fig 7B; 216pp; English.
PS
XX
XX Junction sequences (AA14398-403) are provided of the DNA fragments
CC used to construct homology vector 562-611P, a plasmid designed for
CC the purpose of deleting a 983 bp portion of the glycoprotein gI
CC gene from the unique short region (see also AA14384) of infectious
CC laryngotracheitis virus (ILT), and replacing it with uIdA DNA.
CC The vector incorporates a screenable marker, the E. coli uIdA gene,
CC flanked by ILTV DNA. The homology vector is used to construct
CC attenuated ILTV S-ILT-011, which is useful as a killed vaccine to
CC protect chickens from ILT disease and as a negative marker to
CC distinguish vaccinated from infected animals. It is also used to
CC construct S-ILT-013, which also has a deletion in the gG gene.
XX
SQ Sequence 42 BP; 12 A; 11 C; 8 G; 11 T; 0 other;
Query Match 3.2%; Score 42; DB 17; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 695 CGCAACAGCTCTGTAAGTTCAGAGTTCAGTCTGTT 736
Db 1 CGCAACAGCTCTGTAAGTTCAGAGTTCAGTCTGTT 42
RESULT 11
AAQ21833
ID AAQ21833 standard; DNA: 390 BP.
XX
XX AAQ21833:
AC
XX
XX 08-JUN-1992 (first entry)
DT
XX
XX Randomising oligonucleotide used in SPERT mRNA prepn.
DE
XX
XX Systematic polypeptide evolution by reverse translation; SPERT;
KW ligand binding; ss.
XX
XX Synthetic.
OS
XX
XX W09202536-A.
PN
XX
XX 20-FEB-1992.
PD
XX
XX 01-AUG-1991; 91WO-US05463.
PF
XX
XX 02-AUG-1990; 90US-0561968.
PR
XX
XX (COLS ) UNIV OF COLORADO.
PA
XX
XX Gold L, Tuerk C;
PI
XX
XX WPI: 1992-080018/10.
DR
XX
XX New method of systematic polypeptide evolution by reverse
PT translation - by linking each polypeptide in sample mixt. to
PT individualised mRNA allowing further synthesis of selected
CC
```

```
PT polypeptide(s)
XX
XX Example; Page 55; 102pp; English.
PS
XX
XX The sequence is that of an example randomising oligonucleotide which
CC is used in the prepn. of mRNA encoding candidate polypeptides for the
CC method of systematic polypeptide evolution by reverse translation
CC (SPERT). The method provides a rapid way of isolating and identifying
CC polypeptide ligands which bind to target mols. The polypeptide ligands
CC can be used in e.g. assay methods, diagnostic procedures, cell sorting,
CC as activators or inhibitors of target mol. function, as probes, as
CC sequestering agents, drug delivery vehicles, modifiers of hormone
CC action and as catalysts. See also AAQ21830-Q21832.
XX
SQ Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;
Query Match 3.2%; Score 41.6; DB 13; Length 390;
Best Local Similarity 51.6%; Pred. No. 0.011;
Matches 95; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
QY 1003 GACGACGAAAGCAGGAAAGAGCCCTCCAGAAAGCTCGAGAGCAGNATGACAGCA 1062
Db 201 GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 260
QY 1063 GAGGCTTCTGGAGAAATCTGCGCCCTCCCGAAGACGACGAAATCCCGAGACACC 1122
Db 261 GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 320
QY 1123 GAGCAGATGATCCAAACTCGATCTGACTATTACAATGACATGCCCGCGTATCCG 1182
Db 321 GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 380
QY 1183 GTGG 1186
Db 381 ATGG 384
RESULT 12
AAQ36859
ID AAQ36859 standard; DNA: 390 BP.
XX
XX AAQ36859:
AC
XX
XX 22-JUN-1993 (first entry)
DT
XX
XX PCR primer for 5' fixed sequence contg. T7 promoter and RBS.
DE
XX
XX Systematic peptide evolution by reverse translation; SPERT; ligand;
KW specific; inhibitors; probes; assay; cell sorting; ss.
XX
XX Synthetic.
OS
XX
XX W09303172-A.
PN
XX
XX 18-FEB-1993.
PD
XX
XX 31-JAN-1992; 92WO-US00801.
PF
XX
XX 01-AUG-1991; 91US-0739055.
PR
XX
XX (UYRE-) UNIV RES CORP.
PA
XX
XX Gold L, Prihnow D, Smith JD, Tuerk C;
PI
XX
XX WPI: 1993-076529/09.
DR
XX
XX Systematic polypeptide evolution by reverse translation - used
PT for prodn. of polypeptide ligand specific for desired target
PT molecule
XX
XX Example 1; Page 84; 98pp; English.
CC SPERT is used to select novel polypeptides that bind the antibody
```


OY 327 ATACCTCACTAGGATATCAAGAGGCTGGAGCTGTGCGAGCTCAACCCGATTCTAACGT 386
| | | | | | | | | | | | | | | | | | | | | |
Db 292 GCTCGTGCCACAGGCTTACGGCTTGCAGCGGCCGATCAAGTCAATCATCTGCGG 351
| | | | | | | | | | | | | | | | | | | | | |
OY 387 GGACGACATGATATCGCGGCCAAAGAAAAGAGAGGGGGCCCTTTCGAGGCCCTCCGT 446
| | | | | | | | | | | | | | | | | | | | | |
Db 352 TGCCGACACACACACCGCTACTCCGAGGACGAGCTGCAAGTCTACAGCTGGGGCTGGGG 411
| | | | | | | | | | | | | | | | | | | | | |
OY 447 CGTCTGTTCTACGTGATTAAAGGGGACGACGGCGAGGAC 486
| | | | | | | | | | | | | | | | | | | | | |
Db 412 AGACTTCGGAGGCTGGGGCATGGCAACTCCAGCGACGTC 451
| | | | | | | | | | | | | | | | | | | | | |

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